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OM protein - protein search, using sw model

Run on: July 2, 2003, 16:49:50 ; Search time 15.5397 Seconds  
(without alignments)  
799.016 Million cell updates/sec

Title: US-09-857-583-4

Perfect score: 2283

Sequence: 1 MKSRQALSPLQMEQTDV.....LRYLAVFARMAEQPAGKAL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	631	27.6	457	2	US-08-834-655-2
2	631	27.6	457	3	US-08-834-033A-2
3	631	27.6	457	4	US-09-363-574-2
4	631	27.6	457	4	US-09-363-526-2
5	631	27.6	457	4	US-09-330-235-18
6	631	27.6	458	4	US-09-439-261-10
7	631	27.6	458	4	US-09-439-261-44
8	631	27.6	458	4	US-09-227-613-11
9	631	27.6	458	4	US-09-227-613-41
10	622	27.2	457	2	US-08-833-610-4
11	622	27.2	457	3	US-08-834-033A-14
12	565	24.7	355	2	US-08-834-655-5
13	565	24.7	355	3	US-08-834-033A-6
14	565	24.7	355	4	US-09-363-574-5
15	565	24.7	355	4	US-09-363-526-5
16	524.5	23.0	323	4	US-09-439-261-17
17	524.5	23.0	323	4	US-09-227-613-17
18	461	20.2	452	4	US-09-934-254-27
19	433.5	19.0	448	1	US-08-366-779-5
20	433.5	19.0	448	1	US-08-789-936-5
21	433.5	19.0	448	4	US-08-934-254-5
22	430.5	18.9	446	2	US-08-833-610-5
23	430.5	18.9	446	3	US-08-834-033A-15
24	426	18.7	432	4	US-09-439-261-9
25	426	18.7	432	4	US-09-227-613-9
26	426	18.7	465	4	US-09-439-261-40
27	426	18.7	465	4	US-09-227-613-38

Sequence 11, Appl  
Sequence 12, Appl  
Sequence 39, Appl  
Sequence 45, Appl  
Sequence 43, Appl  
Sequence 42, Appl  
Sequence 19, Appl  
Sequence 18, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 16, Appl  
Sequence 18, Appl  
Sequence 15, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 7, Appl  
Sequence 7, Appl

28 416 18.2 444 4 US-09-439-261-11  
29 416 18.2 444 4 US-09-227-613-12  
30 416 18.2 445 4 US-09-439-261-39  
31 416 18.2 445 4 US-09-439-261-45  
32 402.5 17.6 444 4 US-09-439-261-43  
33 402.5 17.6 444 4 US-09-227-613-42  
34 312.5 13.7 356 4 US-09-439-261-19  
35 312.5 13.7 356 4 US-09-227-613-18  
36 305 13.4 287 4 US-09-439-261-13  
37 305 13.4 287 4 US-09-227-613-13  
38 305 13.4 288 4 US-09-439-261-14  
39 305 13.4 288 4 US-09-439-261-16  
40 305 13.4 288 4 US-09-439-261-18  
41 305 13.4 288 4 US-09-227-613-15  
42 277.5 12.2 252 2 US-08-834-655-7  
43 277.5 12.2 252 3 US-08-834-033A-8  
44 277.5 12.2 252 4 US-09-363-574-7  
45 277.5 12.2 252 4 US-09-363-526-7

#### ALIGNMENTS

#### RESULT 1

US-08-834-655-2

Sequence 2, Application US/08834655

Patent No. 5968809

GENERAL INFORMATION:

APPLICANT: KNUZON, DEBORAH

APPLICANT: MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,655

FILING DATE: 11-APR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RAE-VENTER, BARBARA

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: CGNE.124.0005

TELEPHONE: (650) 328-4400

TELEFAX: (650) 328-4477

TELEX: N/A

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-655-2

Query Match 27.6%; Score 631; DB 2; Length 457;

Best Local Similarity 33.0%; Pred. No. 7.6e-66;

Matches 150; Conservative 76; Mismatches 173; Indels 56; Caps 11;



```
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-574-2

Query Match 27.6%; Score 631; DB 4; Length 457;
Best Local Similarity 33.0%; Pred. No. 7.6e-66;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPQLM--EQTVDVSAWVNFHFGAGAEIENYQGRDATDAFVMVHFQEAFLK 59
DB 23 EGKKADEAPFLMIIDNKVDYREFVDPHGGG-VILTHVGKDGTDVDFTHPEAAWETL- 80
QY 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATCMFDPASPLWYSYKISTT 110
DB 81 -----ANFV---GDIDESDRDIKNDDFAEVFKLTLFQSLGYDSSKAYAFKVSFN 131
QY 111 LGGVLYGYFLMVQYQM-----YFTGAVLLGMHYQOMGLSHDICHQTFKNNMNNLVGL 165
DB 132 LCITWGLSTVIVAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVDFQDFWGDLEGA 191
QY 166 VFCNGLOGSVTCWKDRHNAHHSATNVQGHDPDIDNLPPLANSEDDVTRASPI----- 218
DB 192 FLGGVCGGFSSSWKKDKHNTTHAAPNVHGEDPDIDTHPLTWSEHALEMFSVPDEBLTR 251
QY 219 --SRKLIFQOQYFVLVICILLRFTWCFCQVLTVRSKDRDNQFVRSQYK-----EAIG 270
DB 252 MNSRFVNLQNTWFFPILSFARLSWCLOSILFVLP-----NGQAHKPGCARVPISLVEQLS 307
QY 271 LALHWTLKALFHLFFMPSILTSLLVFFVSELVGGFGIAIVVFMNHYPLEKIGDPVWDG 330
DB 308 LAMHWTWYLATMFLFKIDPVMNLVFLVSAQVCGNLLAIVFSLNHNGMPVISKEEAVDMD 367
QY 331 FSVGQIHTMNIIRGIITDMFFGGLNYQIEHLLWPTLPRNHLTAVSVQVQLCKQHNLPY 390
DB 368 FTKQIITGRDVHPGLFANFTGGLNYQIEHLLFSPMRHNFSKIOPAVETLCKKNVRY 427
QY 391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 4
US-09-363-526-2
; Sequence 2, Application US/09363526
; Patent No. 6410288
; GENERAL INFORMATION:
; APPLICANT: KNUZON, DEBORAH
; APPLICANT: MURKERT, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SONITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-526-2

Query Match 27.6%; Score 631; DB 4; Length 457;
Best Local Similarity 33.0%; Pred. No. 7.6e-66;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPQLM--EQTVDVSAWVNFHFGAGAEIENYQGRDATDAFVMVHFQEAFLK 59
DB 23 EGKKADEAPFLMIIDNKVDYREFVDPHGGG-VILTHVGKDGTDVDFTHPEAAWETL- 80
QY 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATCMFDPASPLWYSYKISTT 110
DB 81 -----ANFV---GDIDESDRDIKNDDFAEVFKLTLFQSLGYDSSKAYAFKVSFN 131
QY 111 LGGVLYGYFLMVQYQM-----YFTGAVLLGMHYQOMGLSHDICHQTFKNNMNNLVGL 165
DB 132 LCITWGLSTVIVAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVDFQDFWGDLEGA 191
QY 166 VFCNGLOGSVTCWKDRHNAHHSATNVQGHDPDIDNLPPLANSEDDVTRASPI----- 218
DB 192 FLGGVCGGFSSSWKKDKHNTTHAAPNVHGEDPDIDTHPLTWSEHALEMFSVPDEBLTR 251
QY 219 --SRKLIFQOQYFVLVICILLRFTWCFCQVLTVRSKDRDNQFVRSQYK-----EAIG 270
DB 252 MNSRFVNLQNTWFFPILSFARLSWCLOSILFVLP-----NGQAHKPGCARVPISLVEQLS 307
QY 271 LALHWTLKALFHLFFMPSILTSLLVFFVSELVGGFGIAIVVFMNHYPLEKIGDPVWDG 330
DB 308 LAMHWTWYLATMFLFKIDPVMNLVFLVSAQVCGNLLAIVFSLNHNGMPVISKEEAVDMD 367
QY 331 FSVGQIHTMNIIRGIITDMFFGGLNYQIEHLLWPTLPRNHLTAVSVQVQLCKQHNLPY 390
DB 368 FTKQIITGRDVHPGLFANFTGGLNYQIEHLLFSPMRHNFSKIOPAVETLCKKNVRY 427
QY 391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 5
US-09-330-235-18
; Sequence 18, Application US/09330235
; Patent No. 6459018
; GENERAL INFORMATION:
; APPLICANT: KNUZON, Debbie
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
; FILE REFERENCE: MOCO 156,00US
; CURRENT APPLICATION NUMBER: US/09/330,235
; CURRENT FILING DATE: 1999-06-10
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Query Match 27.6%; Score 631; DB 4; Length 458;  
Best Local Similarity 33.0%; Pred. No. 7.6e-66;  
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

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QY 2 KSKRQALSPLQIM--EQTYDVSANVNFHPGGAIEIENVOGHDPIDNLPPLAWSEDDVTRASPI-----EAIK 110
DB 23 EGKDAEAPFLMIIDNKYIDVREFVDPHPGGS-VILTHVGKDGTDVDFHPEAAWETL- 80
QY 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSKYSTT 110
DB 81 -----ANFYV---GDIDESDRIKNDFFAAEVRKRLTLFQSLGYDSSKAYIAFKVSFN 131
QY 111 LGLVGLGYFLMVQYQM-----YFICAVLLGMHYQOMGWLSDHCHHOTKRNWNNLVGL 165
DB 132 LCINGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLHDFLHHQVQDFRFGDPLGA 191
QY 166 VFGNGLQGSVTCWKDRNNAHSAATNVQGHDPIDNLPPLAWSEDDVTRASPI-----EAIK 218
DB 192 FLGGVCOGQFSSSSWKKDKHNTHAAPNVHGEDPDIDTHPLLTWSEHALEMFSVDVDELT 251
QY 219 --SRKLIQOQYFYFLVICILLRFTWCFCQVLTVRSKDRDNQFYSQYKK-----EAIK 270
DB 252 MWSRFMVLNQTWTFYFPILSFARLSWCLOSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
QY 271 LALHWTILKALFHLFMPISILTSLVFFVSELVGGGIAIVVFMNHYPLEKIGDPVWDGHC 330
DB 308 LAMHTWYLATMFLFKDPVNMVLYFLVSQAVCGNLLAIVFSLNHNMPVISKEEAVDMD 367
QY 331 FSVGQIHETMIRRIITDWFPGGLNYQIEHHLWPTLPRHNLTAVSQYQVQECOKHNL 390
DB 368 .FFTQKIITGRDVHPCGFANWFTGGLNYQIEHHLFSPMPRHNSKIQPAVETLCKKYNRY 427
QY 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTTGMIETA-----EVFSRLNEVSKAASKMGKA 456
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## RESULT 8

US-09-227-613-11  
; Sequence 11, Application US/09227613A  
; Patent No. 6432684

GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
; FEATURE:  
; OTHER INFORMATION: Xaa at position 458 is unknown or other.  
US-09-227-613-11

Query Match 27.6%; Score 631; DB 4; Length 458;  
Best Local Similarity 33.0%; Pred. No. 7.6e-66;  
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

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QY 2 KSKRQALSPLQIM--EQTYDVSANVNFHPGGAIEIENVOGHDPIDNLPPLAWSEDDVTRASPI-----EAIK 59
DB 23 EGKDAEAPFLMIIDNKYIDVREFVDPHPGGS-VILTHVGKDGTDVDFHPEAAWETL- 80
QY 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSKYSTT 110
DB 81 -----ANFYV---GDIDESDRIKNDFFAAEVRKRLTLFQSLGYDSSKAYIAFKVSFN 131
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QY 111 LGLVGLGYFLMVQYQM-----YFICAVLLGMHYQOMGWLSDHCHHOTKRNWNNLVGL 165
DB 132 LCINGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLHDFLHHQVQDFRFGDPLGA 191
QY 166 VFGNGLQGSVTCWKDRNNAHSAATNVQGHDPIDNLPPLAWSEDDVTRASPI-----EAIK 218
DB 192 FLGGVCOGQFSSSSWKKDKHNTHAAPNVHGEDPDIDTHPLLTWSEHALEMFSVDVDELT 251
QY 219 --SRKLIQOQYFYFLVICILLRFTWCFCQVLTVRSKDRDNQFYSQYKK-----EAIK 270
DB 252 MWSRFMVLNQTWTFYFPILSFARLSWCLOSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
QY 271 LALHWTILKALFHLFMPISILTSLVFFVSELVGGGIAIVVFMNHYPLEKIGDPVWDGHC 330
DB 308 LAMHTWYLATMFLFKDPVNMVLYFLVSQAVCGNLLAIVFSLNHNMPVISKEEAVDMD 367
QY 331 FSVGQIHETMIRRIITDWFPGGLNYQIEHHLWPTLPRHNLTAVSQYQVQECOKHNL 390
DB 368 .FFTQKIITGRDVHPCGFANWFTGGLNYQIEHHLFSPMPRHNSKIQPAVETLCKKYNRY 427
QY 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTTGMIETA-----EVFSRLNEVSKAASKMGKA 456
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## RESULT 9

US-09-227-613-41  
; Sequence 41, Application US/09227613A  
; Patent No. 6432684

GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pradip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; CURRENT FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 41  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
; FEATURE:  
; OTHER INFORMATION: Xaa at position 458 is unknown or other.  
US-09-227-613-41

Query Match 27.6%; Score 631; DB 4; Length 458;  
Best Local Similarity 33.0%; Pred. No. 7.6e-66;  
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

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QY 2 KSKRQALSPLQIM--EQTYDVSANVNFHPGGAIEIENVOGHDPIDNLPPLAWSEDDVTRASPI-----EAIK 59
DB 23 EGKDAEAPFLMIIDNKYIDVREFVDPHPGGS-VILTHVGKDGTDVDFHPEAAWETL- 80
QY 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSKYSTT 110
DB 81 -----ANFYV---GDIDESDRIKNDFFAAEVRKRLTLFQSLGYDSSKAYIAFKVSFN 131
QY 111 LGLVGLGYFLMVQYQM-----YFICAVLLGMHYQOMGWLSDHCHHOTKRNWNNLVGL 165
DB 132 LCINGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLHDFLHHQVQDFRFGDPLGA 191
QY 166 VFGNGLQGSVTCWKDRNNAHSAATNVQGHDPIDNLPPLAWSEDDVTRASPI-----EAIK 218
DB 192 FLGGVCOGQFSSSSWKKDKHNTHAAPNVHGEDPDIDTHPLLTWSEHALEMFSVDVDELT 251
QY 219 --SRKLIQOQYFYFLVICILLRFTWCFCQVLTVRSKDRDNQFYSQYKK-----EAIK 270
DB 252 MWSRFMVLNQTWTFYFPILSFARLSWCLOSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
```





TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-834-033A-6

Query Match 24.7%; Score 565; DB 3; Length 355;  
Best Local Similarity 34.9%; Pred. No. 3.3e-58;  
Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;  
QY 82 DFRKRLRELIATGMDFDASPLWYSYKISTTGLGLVGLYFLVMYQOM-----YFIGAVLLGM 136  
DB 1 EVRKRLTLFOSLGYDSSKAYAFKVSFNLICINGLSTVIIVAKWGQTSITLANVLSAALLGL 60  
QY 137 HYQOMGWLSDICHQHTFKRNNNNLGLVFGNGLQGSFVTCWKDRHNAHHSATNVQGH 196  
DB 61 FWOOCGLAHDFLHQVDFDRFMDLFGAFGLGGVCGGFSWKKDKHNTTHAAPNVHGD 120  
QY 197 PDIDNLPPLAWSDDVTRASPI-----SRKLIQOQYFVLVICILLRFIWCFOCVL 247  
DB 121 PDIDTPLLTHSEHALEMFSDVDEELTRMWSRFVNLQWTFYFPILSFARLSNCLQSIL 180  
QY 248 TVRSLKDRDNOFYSQYKK-----EAIGLALHWTALKALFHLFMPISILSLVFFVSEL 301  
DB 181 FVLP-----NGOAHKPGSGARVPISLVEQLSLAMHWTYLATMFLFKDPVNNLVFLVSA 236  
QY 302 VGGFGIAIVFMNHYHLEKIGDPWDGHSVGOIHEHMTNIRGIIITDWFGLNYQIEH 361  
DB 237 VCGNLLAIVFSLNHGMPVISKEEAVDMDFTKQITIGRDVHPLGFANWFTGGLNYQIEH 296  
QY 362 HLWPTLPRHNLTAVSQVQOLCOQKHNLPYRNPPLPHEGLVILLRYLAVFARMAEKOPA--- 418  
DB 297 HLFPSMRHNFSLKIQPAVETLCKKYNRYHTTGMEGTA-----EVFSRLNEVSKAASK 350  
QY 419 -GKA 421  
DB 351 MGKA 354

RESULT 14  
US-09-363-574-5  
Sequence 5, Application US/09363574  
Patent No. 6136574  
GENERAL INFORMATION:  
APPLICANT: KNUTZON, DEBORAH  
APPLICANT: MURKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THURMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,574  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 30,651  
REFERENCE/DOCKET NUMBER: CGAB-202 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-363-574-5  
Query Match 24.7%; Score 565; DB 4; Length 355;  
Best Local Similarity 34.9%; Pred. No. 3.3e-58;  
Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;  
QY 82 DFRKRLRELIATGMDFDASPLWYSYKISTTGLGLVGLYFLVMYQOM-----YFIGAVLLGM 136  
DB 1 EVRKRLTLFOSLGYDSSKAYAFKVSFNLICINGLSTVIIVAKWGQTSITLANVLSAALLGL 60  
QY 137 HYQOMGWLSDICHQHTFKRNNNNLGLVFGNGLQGSFVTCWKDRHNAHHSATNVQGH 196  
DB 61 FWOOCGLAHDFLHQVDFDRFMDLFGAFGLGGVCGGFSWKKDKHNTTHAAPNVHGD 120  
QY 197 PDIDNLPPLAWSDDVTRASPI-----SRKLIQOQYFVLVICILLRFIWCFOCVL 247  
DB 121 PDIDTPLLTHSEHALEMFSDVDEELTRMWSRFVNLQWTFYFPILSFARLSNCLQSIL 180  
QY 248 TVRSLKDRDNOFYSQYKK-----EAIGLALHWTALKALFHLFMPISILSLVFFVSEL 301  
DB 181 FVLP-----NGOAHKPGSGARVPISLVEQLSLAMHWTYLATMFLFKDPVNNLVFLVSA 236  
QY 302 VGGFGIAIVFMNHYHLEKIGDPWDGHSVGOIHEHMTNIRGIIITDWFGLNYQIEH 361  
DB 237 VCGNLLAIVFSLNHGMPVISKEEAVDMDFTKQITIGRDVHPLGFANWFTGGLNYQIEH 296  
QY 362 HLWPTLPRHNLTAVSQVQOLCOQKHNLPYRNPPLPHEGLVILLRYLAVFARMAEKOPA--- 418  
DB 297 HLFPSMRHNFSLKIQPAVETLCKKYNRYHTTGMEGTA-----EVFSRLNEVSKAASK 350  
QY 419 -GKA 421  
DB 351 MGKA 354

RESULT 15  
US-09-363-526-5  
Sequence 5, Application US/09363526  
Patent No. 6410288  
GENERAL INFORMATION:  
APPLICANT: KNUTZON, DEBORAH  
APPLICANT: MURKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THURMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-526-5

Query Match      24.7%; Score 565; DB 4; Length 355;
Best Local Similarity 34.9%; Pred. No. 3.3e-58;
Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;

Qy 82 DFRKRLRELIATGMFDASPLWYSKISTTIGLGLVGLVFLWVQYQ-----YFIGAVLLGM 136
Db 1 EVKRLTLFQSLGYDSKAYAFKVSFNLCIWLSTVIVAKWGQSTLANVLSAALLGL 60

Qy 137 HYQMGWLSHDICHQTFKNNWNNLVGLVFGNGLQGFSVTCWKDRHNAHSAATNVQGH 196
Db 61 FWOQCGWLHDFLHQVFQDRFGDLFGAFLGGVCGQGFSSSWKDKNTHHAAPNVHGED 120

Qy 197 PDIDNLPPLAWSEDDVTRASPI-----SRKLIQFQYYFLVICILLRFWCFCQVL 247
Db 121 PDIDTHPLLTWSEHALENFSDVDPDELTRMWSRFMVLNQTWFFPILSFARLSWCLQSIL 180

Qy 248 TVRSLKDRDNQFYRSQYKK-----EALGLAHWTLKALPHLEFMPSTLTSLLVFFVSEL 301
Db 181 FVLP-----NGAHPFGARVPISLVEQLSLAHHTWYLATWFLFKDPVNMVFLVLSQA 236

Qy 302 VGGEGIAIVVPMNHYPLEKIGDPVWDGHGFSVGQIHEMTNIRGIIITDWFEGGLNYQIEH 361
Db 237 VCGNLLAIVFSLNHGMPVISKEEAVDMDFTKLIITGRDVHPGLFANWFTGGLNYQIEH 296

Qy 362 HLWPTLPRHNLTAYSQVEQLCQKHNLPYRNPPLPHEGLVILLRYLAVFARMKQPA--- 418
Db 297 HLFPSMPRHPNFSKIOPAVETLCKKYNRYHTTGMIEGTA-----EVSRLNEYSKAASK 350

Qy 419 -GKA 421
Db 351 MGKA 354
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Search completed: July 2, 2003, 19:28:45  
Job time : 17.5397 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 19:20:22 ; Search time 29.6226 Seconds  
(without alignments)  
1638.178 Million cell updates/sec

Title: US-09-857-583-4  
Perfect score: 2283  
Sequence: 1 MKSKRQALSPQLMEQTYDV.....LRYLAVFARMAEKOPAGKAL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	27.6	458	9	US-10-191-513A-11
2	631	27.6	458	9	US-10-191-513A-41
3	601	26.3	459	9	US-09-967-477B-8
4	524.5	23.0	323	9	US-10-191-513A-17
5	461	20.2	452	12	US-10-029-756-27
6	443.5	19.4	445	9	US-10-262-617-1
7	433.5	19.0	448	12	US-10-029-756-5
8	430	18.8	444	9	US-10-262-617-3
9	426	18.7	432	9	US-10-191-513A-9
10	426	18.7	465	9	US-10-191-513A-38
11	416	18.2	444	9	US-10-191-513A-12
12	402.5	17.6	444	9	US-10-191-513A-42
13	372	16.3	439	9	US-09-967-477B-4
14	312.5	13.7	356	9	US-10-191-513A-18
15	310	13.6	286	9	US-10-102-806-650
16	305	13.4	287	9	US-10-191-513A-14
17	305	13.4	288	9	US-10-191-513A-15
18	295.5	12.9	353	9	US-10-156-761-9130
19	286	12.5	456	9	US-09-967-477B-6

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20 275 12.0 360 9 US-10-191-513A-39
21 270.5 11.8 365 9 US-10-156-761-9835
22 249.5 10.9 446 10 US-09-903-456-30
23 249.5 10.9 447 9 US-10-191-513A-10
24 239 10.5 359 12 US-10-029-756-2
25 233.5 10.2 347 9 US-10-191-513A-40
26 211.5 9.3 515 9 US-09-849-199A-18
27 211.5 9.3 515 9 US-09-849-199A-19
28 207.5 9.1 515 9 US-09-849-199A-20
29 203.5 8.9 515 9 US-09-849-199A-21
30 200 8.8 519 9 US-09-967-477B-2
31 190.5 8.3 315 9 US-10-191-513A-16
32 184 8.1 370 10 US-09-815-242-5200
33 177.5 7.8 219 9 US-10-191-513A-19
34 149 6.5 383 10 US-09-837-751-6
35 140 6.1 387 9 US-09-981-124-13
36 140 6.1 387 9 US-10-224-446-5
37 140 6.1 387 10 US-09-837-751-33
38 139.5 6.1 335 9 US-09-849-199A-26
39 138.5 6.1 384 10 US-09-995-297-8
40 137.5 6.0 384 9 US-09-981-124-10
41 137.5 6.0 384 10 US-09-995-297-6
42 135 5.9 182 9 US-10-191-513A-20
43 134.5 5.9 383 10 US-09-837-751-31
44 134.5 5.9 384 10 US-09-885-188-4
45 134.5 5.9 384 10 US-09-885-189-4
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## ALIGNMENTS

## RESULT 1

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US-10-191-513A-11
; Sequence 11, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/933,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-11
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## Query Match

Best Local Similarity 27.6%; Score 631; DB 9; Length 458;

Matches 150; Conservativity 33.0%; Pred. No. 3.9e-57;

Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPQLM--EQTVDYSAWYFNHPGGEIENYQGRDADFVYMHFQAEADK 59

Db 23 EGKDKAEAPFLMIIDNKVDYDFVDPHPGGS-VILTHVGKDGTDVDFHFEAAWETL- 80

QY 60 RMPKINPSEFLPPQAAVNEAQEDF-----RKLRLELIATGMFDASPLWYSYKISTT 110



Db 305 DGPEKAGLVHYIWLAIYFCNMSLPGVAYFLMQASCGLLLALVFSIGHNGMSYTER 364  
Qy 319 EKIGDPVWDGHSVQGIHETMNRIRGITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQY 378  
Db 365 ETKPD-----FQLOQVTTTRNIRASVFMDFGTGGLNYQIDHHLFLPLVPRHNLPKVNL 417  
Qy 379 VEOLCOKHNLPRNPLPHEGLVILLRYLA 407  
Db 418 IKSCKEFDIPFHETGFWEGYEVVDHLA 446

## RESULT 4

US-10-191-513A-17  
; Sequence 17, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Paridip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191-513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (323)...(323)  
; OTHER INFORMATION: Xaa - Unknown or other at position 323  
US-10-191-513A-17

Query Match 23.08; Score 524.5; DB 9; Length 323;  
Best Local Similarity 36.9%; Pred. No. 3e-46;  
Matches 115; Conservative 45; Mismatches 123; Indels 29; Gaps 5;  
Qy 129 IGAVLLGMHYQMGWLSHDICHOTFKNRNNNLVGLVFGNGLOGESVTCCKDRHNAHS 188  
Db 20 LSAALLGFWQCCGWLADHLHGVFQDRFGWDLFGAFLGVCGGFGSSWWKDKHNTHA 79  
Qy 189 ATNVQGHDPDIDNPLPLAWSDDVYTRASPI-----SRKLQFOQYYFLVICILRF 239  
Db 80 APNVHGEDPDIDTHTPLTWSEHALEMFSVDEELTRWSRFVNLQWTFYFPLSARL 139  
Qy 240 IKFCQCVLTVRSKDRNQVRSQYK-----BAIGLALHWTALKALFLHFFMPSILTS 293  
Db 140 SWCLOSLTLFVLP-----NGAHPKPGARVPSLSVQLSLAMHWTYLATMFLFKIDPVNML 195  
Qy 294 LVFEVSELVGGFGTAIVVFNHYPLEKIGDPVWDGHSVQGIHETMNRIRGITDWF 353  
Db 196 VYFLVSAVCGNLLAIIVLSLNHNGMPVISKEEAVDMDFFTKQIITGRDVPGLFANFTG 255  
Qy 354 GLNAYQIEHHLWPTLPRHNLTAVSQVQEQLOKKNLPRNPLPHEGLVILLRYLAFAARMA 413  
Db 256 GLNAYQIEHHLFSPMRNFSKIQPAVETLCKKNVRYHTTGMIETGTA-----EVFSRLN 309  
Qy 414 EKQPA-----GKA 421  
Db 310 EVSKAASKMGKA 321

## RESULT 5

US-10-029-756-27  
; Sequence 27, Application US/10029756  
; Patent No. US20020108147A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; DELTA 6-DESATURASE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/029,756  
; FILING DATE: 21-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/934,254  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-10-029-756-27

Query Match 20.2%; Score 461; DB 12; Length 452;  
Best Local Similarity 27.6%; Pred. No. 2e-39;  
Matches 123; Conservative 73; Mismatches 189; Indels 60; Gaps 10;  
Qy 11 LQLEQTYDVSANVNFHFGGAEIENYQGRDATDAFVMVHFOEADKLRMPKINPSFEL 70  
Db 25 ISIQGVYDCSRWAAEHGPEVPLLSLAGQDVTDAFIAYHPTAW---RHLDPLFTGYTY 81  
Qy 71 PPQAAVNEAQEDFRKLRELIATGMEDASP---LWYSYKISTTLGLGLVGLYFLMWQYQW 127  
Db 82 LKDFEVSISDKYRRLNEMSRGIFKKGHIMMTFVGVAVYMAAIVTVGLASESVGVH 141  
Qy 128 FIGAVLLGMHYQMGWLSHDICHOTFKNRNNNLVGLVFGNGLOGESVTCCKDRHNAHS 187  
Db 142 MLCGALLGLLWLTQAYVGHDSGHYQVMPTRGYNRITQIAGNLLTGISTAWKWTNNAH 201  
Qy 188 SATNVQGHDPDIDNPLPLAWS-----DDVTRASPISRKLQFOQYYFLVICIL 236  
Db 202 LACNSLDYDPLDQHIFPAVSTRFNSITSFVGRVLKDFEARELVSHQWYTYVPMIF 261  
Qy 237 LR---FWCFOCVLTVRSKDRNQVRSQYKKEAIGLALHWTALKALFLHFFMPSILTS 293  
Db 262 GRVNLFIQTFFLLTLTRDVPDR-----ALNLMGIAVETWTFPLF----- 300  
Qy 294 LVFEVSELVGGFGTAIVVF-----MNHYPLEK-IGDPVWDGHSVQGIHETM 341  
Db 301 -VSCLPNWPERFGVFLISFAVTAIQHVQFTLNHFSGDYVGPDP---KGNWFKEKGTID 357  
Qy 342 IRRGIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVQEQLOKKNLPRN---PLPHE 397



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Db      358   ITCCPPMDFWFFGGLQFLEHLFLPKLPRGQLRKTAPLARDLCKKHGMYPESFGFWDDANV 417
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Qy      398   GVIILLRYLANVEARMAEQPAGKAL 422
          : || || || || || || || || || || || || || || || || || || || ||
          +-----+-----+-----+-----+-----+-----+-----+-----+
Db      418   RTIRTLDRDAAVQARDNSAPCPKKL 442
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RESULT 6
US-10-262-617-1
; Sequence 1, Application US/10362617
; Publication No. US20030077747A1
; GENERAL INFORMATION:
; APPLICANT: Hallman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PF-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262,617
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 09/048,888
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030077747A1 2451043CD1
US-10-262-617-1

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[illegible]

RESULT 7  
US-10-029-756-5  
; Sequence 5, Application US/10029756  
; Patent No. US20020108147A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
DELTA 6-DESATURASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLY APPLICATION NUMBER: US/10/029,756  
FILING DATE: 21-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLY APPLICATION NUMBER: 08/934,254  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 83832YXWVU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 448 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-029-756-5

Query Match	19.08;	Score	433.5;	DB	12;	Length	448;		
Best Local Similarity	29.98;	Pred.	No. 1.5e-36;						
Matches	121;	Conservative	67;	Mismatches	167;	Indels	51;	Gaps	14;

  

Qy	11	LQLMEQTDYSANVNFHPGGAETIENYQGRDATDAFVMVHFQEAADFCLKRMPKINPSPFEL	70
Db	25	ISIQKRAYDSQDMWKDHPPGGSPFLKSLAGQEVDAFVAFHPASTW---KNLDREFTGYL	81
Qy	71	PPQAAVNEAQDEFRKLREELIATIGMFEA-----SPLWYSYKISTITLGLGVGLVFLMVQY	123
Db	82	KDYSYSEVSKDYRLKLVFEFSKMGLYDKKGHMFATLCF--IAMLFAMSVYGVLFCEGV	137
Qy	125	QMTFIGAVLLGMHYQMGWLUSDHICHHQTEKFNRRNNWNLVGLVFGNGLOGQSVTCWKDRHN	184
Db	138	LVHLFGCLMGFLWIOSGTGHDAGHYMYVSDSLRNFKNMFIFANCISGISIGWKKWNHN	197
Qy	185	AHSAATNVQGHDPDINDLPLAWS-----EDDVTRASPISRKLIQFOQYYFLV	232
Db	198	AHHIACNSLEYDDPLQVLPVLYSSFFGSLTSHFYEKRLTFDS-LSRFFVSQYHWTYP	256
Qy	233	ICILLRFTWFCQVLTVRSUKDRDNQFYRSQYKKEAIGLALHMTLKAFLHFLFFMPSILTS	292
Db	257	IMCAARLNNYVQSLI--MLLTRNNYSYRAQ---ELLGC-----LVFSIWY--PLLVS	301
Qy	293	LL-----VFFSVELVGGFGIAIVFP-MNHYPLE-KIGDPVWDGHGFSVQIHEWTMIRR	344
Db	302	CLPNWGERIMFVIASLTASVGMQVQFSLNHFSSVYVKGK--KGNWNFEKOTDGTGLDISC	359
Qy	345	GIITDNFFGGLNQIEHHLWPTLPRLNHLTAVSYQVEOLCCKHNLPY	390
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RESULT	8
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; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (432)...(432)
; OTHER INFORMATION: Xaa - Unknown or other at position 432
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa - Unknown or other at position 458
US-10-191-513A-38

Query Match      18.7%; Score 426; DB 9; Length 465;
Best Local Similarity 28.0%; Pred. No. 9.5e-36;
Matches 118; Conservative 72; Mismatches 178; Indels 54; Gaps 12;

Qy 11 LQMEQYDVSANVNFHGGAEIETNYOGRDATDAFVMVHFOEAFDK-----LKRMPK 63
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 LVDRKYNINSEFTRRHGGSRVISHYAGODATDPFAFHINKGLVKYKMNLLIGELSP 83
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 64 INPSFELPPQAAVNEAQEDFRKLREELIATGMFASPLWYSYKI-----STTLGLGV 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 84 EQPSFE---PTKNKELTDEFRELRTATVERMGLMKANHVFFLLYLLHLLDGAAWLTLMV 140
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 116 LGYFLMVQYMYFTGAVLLGHYQOMGWLSDHCHHOTFKNNRNNNLVGLVFGNGLOGFS 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 141 FG-----TSFLPFLCAVLLSAVQAQAGWLQHDYGLHSYRKPKNHLVHKEVIGHLKAS 196
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 176 VTCWKDRNNAHNSATNVQGHDPDIDNLPPLAWSDDVTRASPI---SRKLIQF-----QQ 227
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 ANMNNHRHFQHAKEPNIFHKDPDYNMLHVFVLGE-----WQPIEVGKKKLYLPYNHQHE 251
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 228 YYELV-ICILRFIWCFCVLTVRSKLDRDNQFYRSQYKKEAIGALHWTLKALPHLFPM 286
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 252 YFFLIGPLPMTFOYQIINTM-----IVHKNVWDLAWAVSYIRFFITIYI 298
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 287 P--SILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDGHSVGOIHETMNR 344
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 PFYIGLALLFLNIRFLESWFVWVYTMNHIWDEQAEYED--WFS-SQLTATCNVEQ 355
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 345 GIITDFGGLNYQIEHHLWPTLPRHNLTAVSQVQEQLCQKHNLPRNPLPHEGLVILLR 404
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 SFENDWFSGLNFQIEHHLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIR 415
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 405 YL 406
   |
Db 416 SL 417

RESULT 11
US-10-191-513A-12
; Sequence 12, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa - Unknown or other at position 444
US-10-191-513A-42

; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa - Unknown or other at position 444
US-10-191-513A-42

Query Match      18.2%; Score 416; DB 9; Length 444;
Best Local Similarity 28.5%; Pred. No. 9.9e-35;
Matches 117; Conservative 66; Mismatches 174; Indels 54; Gaps 14;

Qy 11 LQMEQYDVSANVNFHGGAEIETNYOGRDATDAFVMVHFOEAFDK-----LKRMPK 63
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 LVDRKYNINSEFTRRHGGSRVISHYAGODATDPFAFHINKGLVKYKMNLLIGELSP 95
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 64 INPSFELPPQAAVNEAQEDFRKLREELIATGMFASPLWYSYKI-----STTLGLGV 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 EQPSFE---PTKNKELTDEFRELRTATVERMGLMKANHVFFLLYLLHLLDGAAWLTLMV 152
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 116 LGYFLMVQYMYFTGAVLLGHYQOMGWLSDHCHHOTFKNNRNNNLVGLVFGNGLOGFS 174
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 FG-----TSFLPFLCAVLLSAVQAQAGWLQHDYGLHSYRKPKNHLHFFVIGH-LKGA 207
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 175 SVTCWKDRNNAHNSATNVQGHDPDIDNLPPLAWSDDV--TRASPISRKLIQF---QOY 229
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 208 PASMNNHMFQHAKEPNIFHKDPDYNMLHVFVLGE-----WQPIEVGKKKLYLPYNHQHE 266
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 230 FLV---ICILRFIWCFCVLTVRSKLDRDNQFYRSQYKKEAIGALHWTLKALPHLFPM 286
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 267 FLIGPPALLPLFYQWYI-----FYFVIQRKKVWDLAWMITFVYRFFLTIV 311
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 287 P--SILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDGHSVGOIHETMNR 344
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 312 PLLGLKAFGLFFIVRFLESNFWVWVYTMNHIWDEQAEYED--WVSTQLLATCNVHK 368
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 345 GIITDFGGLNYQIEHHLWPTLPRHNLTAVSQVQEQLCQKHNLPRNPLPHEGLVILLR 394
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 369 SAFNDWFSGLNFQIEHHLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIR 419
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-10-191-513A-42
; Sequence 42, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa - Unknown or other at position 444
US-10-191-513A-42
```

Query Match 17.6%; Score 402.5; DB 9; Length 444;  
Best Local Similarity 28.2%; Pred. No. 2.5e-33;  
Matches 116; Conservative 65; Mismatches 175; Indels 55; Gaps 14;

QY 11 LQLEQTYDYSANWFHPPGAEIENYQGRDATDAFMMHFQAEAFDK-----LKRMPK 63  
DB 36 LVDRKYNINSEFRRHPGGSRVISHYAGQDADPPFAFHINKGLVKYKNSLLIGELSP 95

QY 64 INSEFELPPAAVNEAQEDFRKLREELIATGMDASPLWTSYKI-----STTIGLV 115  
DB 96 EOPSFE-----PTNKELTDEFELRATVERGLMKANHVFFLLYLLHLLLDGAWLTLW 151

QY 116 LGYFLVQYOMYFIGAIVLLGHYQOMGLSHDICHHTQFNKRNNWNLV-GLVFGNGLOGF 174  
DB 152 FG-----TSFLPFLCALVLLSAVQAQAGLQHDGSLVSFTSKNHLHLHFVIGH-LKGA 206

QY 175 SVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDV--TRASPISRKLIQF---QOYY 229  
DB 207 PASWNNHMFQHHAKPNCFRKDPDI-NMHPFFALGKILSVELGKQKKYMPYNHQQHYF 265

QY 230 FLV---ICILLRIWFOCVLTVRSKDRDNQYRSQYKKEAIGLALHWTLKALFLHFFM 286  
DB 266 FLIGPPALLPLXYQWYI-----EYFVIQRKKWVDLAWMITFYVRFFLTYY 310

QY 287 P--SILTSLLVFFVSELVGGFGIAIVVMNHYPLEKIGDPVWDGHSVQCIHETMNR 344  
DB 311 PLGLKAFGLFFIVFLESNWFVWVTQMNHPIHMDHNRMD---WVSTQLLATCNVHK 367

QY 345 GIITDFFGGLNYQIEHHLWPTLRNHLTAVSQVQEQOLCOKHNLPRN-PL 394  
DB 368 SAFNDWFSGLHNFQIEHHLWPTLRNHLTAVSQVQEQOLCOKHNLPRN-PL 418

RESULT 13  
US-09-967-477B-4  
; Sequence 4, Application US/09967477B  
; Patent No. US30020156254A1  
; GENERAL INFORMATION:  
; APPLICANT: Xiao Qiu  
; APPLICANT: Haiping Hong  
; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL  
; FILE REFERENCE: BZ-001  
; CURRENT APPLICATION NUMBER: US/09/967,477B  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/236,303  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/297,562  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 439  
; TYPE: PRT  
; ORGANISM: Thraustochytrium sp.  
US-09-967-477B-4

Query Match 16.3%; Score 372; DB 9; Length 439;  
Best Local Similarity 29.2%; Pred. No. 3.8e-30;  
Matches 121; Conservative 69; Mismatches 164; Indels 60; Gaps 21;

QY 18 YDVSANWFN-HPGGAEI---IENYQGRDATDAFMMHFQ--EAFDKLRMPKINPS---- 67  
DB 33 YDAT---NEKHPGGSIIINTEGEACVATQAYREPHRSGKADYKLSPLKLDASKVES 89

QY 68 -FELPPQAAVNEAQEDFRKLREELIATGMDASPLWTSYKI---STTIGLVFLVQYQ- 125  
DB 90 REFAKEQARRDAMTDYAAFAREELVAEGYFDPISPHMIYRVVEIVAFALFALSMKASP 149

QY 126 -MYFTGAVLLGHYQOMGLSHDICHHTQFNKRNNW--NNLVGLVFGNGLOGESVTCWKDR 182  
DB 150 TSLVLGVNNGIAQRCGVMHHEM-GHGSFTGTGVILDDRMCEFFYGVGC-GMSGHYWKNO 207

QY 183 HNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASP--ISRKLIQFOQYFVL-VICILLRF 239  
DB 208 HSKHHAAPNRLEHVDLNTLPLVAFNERVRKVPKPGSLALWLRLVQAYLFAVPVSCLLIGL 267

QY 240 IWCFOCVLTVRSKDRDNQYRSQYKKEAIGLALHWTLKALFLHFFMPSIL-----TSLL 294  
DB 268 GW-----TLYLHPRYMLRTRHMEFV-----WIFARYIGFSLMGALGYSPTSGV 313

QY 295 VFFVSELVGGFGI-AIVFM-----NHYPLEKIGDPVWDGHSVQCIHETMNT-RRGI 346  
DB 314 MYLCS-----FGLGCIIVFLQFAVSHTHLPVTNPEDQL---HWLEYAADH-TVNISTKSW 364

QY 347 ITDFFGGLNYQIEHHLWPTLRNHLTAVSQVQEQOLCOKHNLPRNPLPHGELV 400  
DB 365 LVTWMSNLNFAQIEHHLWPTLRNHLTAVSQVQEQOLCOKHNLPRNPLPHGELV 417

RESULT 14  
US-10-191-513A-18  
; Sequence 18, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardiip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 356  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (294)....(294)  
; OTHER INFORMATION: Xaa = Unknown or other at position 294  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (320)....(320)  
; OTHER INFORMATION: Xaa = Unknown or other at position 320  
US-10-191-513A-18

Query Match 13.7%; Score 312.5; DB 9; Length 356;  
Best Local Similarity 30.2%; Pred. No. 4.5e-24;  
Matches 87; Conservative 48; Mismatches 122; Indels 31; Gaps 8;

QY 129 IGAVLLGMHYQOMGLSHDICHHTQFNKRNNWNLVGLVFGNGLOGFSVTCWKDRHNAHS 188  
DB 13 ITAFVLATSDQAQAGLQHDYGLSVYKPKRNHLVHKFVIGHLKAGANWNNHRRFQHHA 72

QY 189 ATNVQGHDPDIDNLPPLAWSEDDVTRASPI--SRKLIQF-----QOYFVLV-ICILLRF 239  
DB 73 KPIEFKDPDNNLHVFLGE-----WQPIEYKGGKKLKLKLPYNHQQHEVFFLIGPPLIPM 127

QY 240 IWCFOCVLTVRSKLD-RDNQYRSQYKKEAIGLALHWTLKALFLHFFMPSILTSLLVFFV 298  
DB 128 YFOYQIIMTIVHKNWVDLAWAVSYIRFTTIPFYGILGALLFLNIRFLESHWFMV-- 185

QY 299 SELVGGFGIAIVVMNHYPLEKIGDPVWDGHSVQCIHETMNTIRRIITDWFPGGLNYQ 358  
DB 186 -----VTQMNHIVMEIDQEAIRD--WFS-SQLTATCNVEQSFNDWFSGLHNFQ 231



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	62.4	4.3	449	9	US-10-191-513A-37	Sequence 37, Appl
2	62.4	4.3	473	9	US-10-191-513A-36	Sequence 36, Appl
3	62.4	4.3	655	9	US-10-191-513A-3	Sequence 3, Appl
4	62.4	4.3	864	9	US-10-191-513A-13	Sequence 13, Appl
5	62.4	4.3	1335	9	US-10-191-513A-1	Sequence 1, Appl
6	62.4	4.3	1928	9	US-10-262-617-4	Sequence 4, Appl
c	62.4	4.3	1972	10	US-09-822-849A-485	Sequence 485, App
7	62.4	4.3	1928	9	US-10-191-513A-6	Sequence 6, Appl
8	58.6	4.0	1474	9	US-10-191-513A-7	Sequence 7, Appl
9	58.6	4.0	1685	9	US-10-191-513A-8	Sequence 8, Appl
10	58.6	4.0	1843	9	US-10-191-513A-355	Sequence 355, App
11	58.6	4.0	2257	9	US-09-902-941-355	Sequence 355, App
c	52	3.6	347	9	US-09-736-457-355	Sequence 355, App
12	52	3.6	347	9	US-09-902-941-355	Sequence 355, App
13	52	3.6	347	9	US-09-736-457-355	Sequence 355, App
c	52	3.6	347	9	US-09-736-457-355	Sequence 355, App
14	52	3.6	347	9	US-09-736-457-355	Sequence 355, App
15	52	3.6	347	9	US-09-736-457-355	Sequence 355, App
c	52	3.6	347	9	US-09-736-457-355	Sequence 355, App
16	52	3.6	347	9	US-10-017-754-355	Sequence 355, App
c	52	3.6	347	9	US-10-017-754-355	Sequence 355, App
17	52	3.6	347	9	US-10-040-862-4558	Sequence 4558, App
c	52	3.6	1717	9	US-10-262-617-2	Sequence 2, Appl
18	51.8	3.5	1059	9	US-10-156-761-1580	Sequence 1580, App

db	182	CAGCTCCAGGCACATGCATGTCCACAAGTCTGCCTTCAATGACTGGTTTCAGTGGACAC	241
Qy	1183	CTTAACATATCAGATTGACGACCACTTTTCCCAACAGATGCCACGACACAACTTGAACACT	1242
db	242	CTCAATTTTCAGATTGAGCACCATCTTTTCCCAACAGATGCTCGACCAATTACCACAA	301
Qy	1243	GTATGCCACTTCTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCTGA	1298
db	302	GTGGCTCCCTGTGGAGTCCTTGTGTGCCAAGCATGGCATGAGTACCAAGTCCAA	357

## RESULT 2

```

US-10-191-513A-36
; Sequence 36, Application US/10191513A
; Publication NO. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: mukerji, pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295. US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-36

```

	Query Match	4.3%	Score 62.4;	DB 9;	Length 473;
	Best Local Similarity	59.7%;	Pred. No. 1.9e-06;		
	Matches 105; Conservative	0;	Mismatches 71;	Indels	Gaps 0;
Qy	1123	CAAATCATGACCAAGAAATATGAGACCCTGGGAAGATTTCATTCAGCTGGCTTTGGGGAGGT	1182		
Dd	213	CAGCTCCTGCCACATGCAATGTCACAACCTTGCCCTTCAATGACTGGTTTCAGTGGGACAC	272		
Qy	1183	CTTAACTATCAGATTGAGCACCATCTTTTTCCCACAGATGCAGACACAACTTGAACACT	1242		
Dd	273	CTCAACTTCCAGATTGAGCACCATCTTTTTCCACAGATGCCTCGACACAAATTACCAAAA	332		
Qy	1243	GTATGCCACTGTTAAGGAGTTTGCAGCAGCAAATGGTTTACCATAATACATGGTCGA	1298		
Dd	333	GTGGCTCCCCGTGGTGCAGTCTTTGTGTGCCAAGCGTGGCATAGAGTACCAAGTCCAA	388		

### RESULT 3

```

US-10-191-513A-3
; Sequence 3, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295. US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422

```

```

; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-3

```

	Query Match	4.3%	Score 62.4	DB 9	Length 655
	Best Local Similarity	59.7%	Pred. No. 2.3e-06		
	Matches 105	Conservative	0	Mismatches 71	Indels 0
Qy	1123	CAAAATCATGACCAAGAATAATGAGACCTGGAGAAGATTCATTCACTGGCTTTGGGGAGGT	1182		
Db	176	CAGCTCCAGGCCACATGCAATGTCACAGCTCGCCTTCATCAATCACTGGTTCAGTGGACAC	235		
Qy	1183	CTTTAACTATCAGATTGAGCACCATTCTTTTCCCAACATGCCAGCAGACAACTTTGAACACT	1242		
Db	236	CTCAACTTCAGATTGAGCACCATTCTTTTCCCAACATGCTCTCGACACAATTACCCACAA	295		
Qy	1243	GTATTGCCACTTGTTAAGAGTTTGGCAGCAGCAAAATGGTTTACCATACATGGTCTGA	1298		
Db	296	GTGGCTCCCTCGTGGCAGCTCTGTGTGGCAACGATGGCATAGAGTACCAAGTCCAA	351		

## RESULT 4

```

US-10-191-513A-13
; Sequence 13, Application US/10191513A
; Publication NO. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191.513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-191-513A-13

```

	Query Match	4.3%	Score 62.4	DB 9	Length 864
	Best Local Similarity 59.7%	Pred. No. 2.7e-06			
	Matches 105	Conservative 0	Mismatches 71	Indels 0	Gaps 0
QY	1123	CAAAATCATGACCAAGCAAGAAATATGAGACCTGGAGATTCATTCACCTGGCTTTGGGGAGGT	1182		
DB	604	CAGCTCAGGCCACATGCATGTCACAACTGCGCTTCATGACTGGTTCAGTGGGACAC	663		
QY	1183	CTTAACTATCAGATTGGACACCATCTTTTCCCAACGATGCCAGCGACACACTTTGAACACT	1242		
DB	664	CTCAACTTCAGATTGGACACCATCTTTTCCCAACGATGCCTCGACACATTACCCACAA	723		
QY	1243	GTTATGCGCACTGTTTAAAGGAGTTTGGCAGCAGCAAAATGGTTTACCATACATGTTGCA	1298		
DB	724	GTGGCTCCCTGGTGGCAGTCTCTTGTGTGCCAAGCATGGCATAGACTAGTACCACTGCA	779		

## RESULT 5

US-10-191-513A-1  
; Sequence 1, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardi  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-191-513A-1

Query Match 4.3%; Score 62.4; DB 9; Length 1335;  
Best Local Similarity 59.7%; Pred. No. 3.5e-06;  
Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
QY 1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTTCATTGACTGGCTTTGGGGAGGT 1182  
DB 1075 CAGCTCCTGCCACATGCAATGCCACAAGTCTGCTTCAATGACTGGTTCAGTGGACAC 1134  
QY 1183 CTTAATCATGAGATTGAGCACCATTCTTTCCCAACAGTGCACGACGACGACACTTGACACT 1242  
DB 1135 CTCACCTCCAGATTGAGCACCATTCTTTCCCAACAGTGCCTCGACACAAATTACCAAAA 1194  
QY 1243 GTTATGCCACTTGTAAAGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCCA 1298  
DB 1195 GTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCGTGGCATAGTACCAAGTCCAA 1250

## RESULT 6

US-10-262-617-4  
; Sequence 4, Application US/10262617  
; Publication No. US20030077747A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-5 DESATURASE HOMOLOGS  
; FILE REFERENCE: PF-0494-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/262,617  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 09/048,888  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 1928  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20030077747A1 2056310CB1  
US-10-262-617-4

Query Match 4.3%; Score 62.4; DB 9; Length 1928;  
Best Local Similarity 59.7%; Pred. No. 4.4e-06;

Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
QY 1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTTCATTGACTGGCTTTGGGGAGGT 1182  
DB 1158 CAGCTCAGGCCACATGCAATGTCCACAAGTCTGCCCTTCAATGACTGGTTCAGTGGACAC 1217  
QY 1183 CTTAATCATGAGATTGAGCACCATTCTTTCCCAACAGTGCACGACGACGACACTTGACACT 1242  
DB 1218 CTCACCTCCAGATTGAGCACCATTCTTTCCCAACAGTGCCTCGACACAAATTACCAAAA 1277  
QY 1243 GTTATGCCACTTGTAAAGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCCA 1298  
DB 1278 GTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCATGGCATAGTACCAAGTCCAA 1333

## RESULT 7

US-09-822-849A-485/c  
; Sequence 485, Application US/09822849A  
; Patent No. US20020045170A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulkota, Kamalakar  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6403  
; CURRENT APPLICATION NUMBER: US/09/822,849A  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/195,582  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 598  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 485  
; LENGTH: 1972  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-822-849A-485

Query Match 4.3%; Score 62.4; DB 10; Length 1972;  
Best Local Similarity 59.7%; Pred. No. 4.5e-06;  
Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTTCATTGACTGGCTTTGGGGAGGT 1182  
DB 808 CAGCTCAGGCCACATGCAATGTCCACAAGTCTGCCCTTCAATGACTGGTTCAGTGGACAC 749  
QY 1183 CTTAATCATGAGATTGAGCACCATTCTTTCCCAACAGTGCACGACGACGACACTTGACACT 1242  
DB 748 CTCACCTCCAGATTGAGCACCATTCTTTCCCAACAGTGCCTCGACACAAATTACCAAAA 689  
QY 1243 GTTATGCCACTTGTAAAGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCCA 1298  
DB 688 GTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCATGGCATAGTACCAAGTCCAA 633

## RESULT 8

US-10-102-806-232  
; Sequence 232, Application US/10102806  
; Publication No. US20030054421A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103P1C1  
; CURRENT APPLICATION NUMBER: US/10/102,806  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 09/925,298  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05981



;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR APPLICATION NUMBER: 60/124,270  
;; PRIOR FILING DATE: 1999-03-12  
;; NUMBER OF SEQ ID NOS: 846  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 232  
;; LENGTH: 1474  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1337)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1359)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1377)  
;; OTHER INFORMATION: n equals a,t,g, or c  
US-10-102-806-232

Query Match 4.0%; Score 58.6; DB 9; Length 1474;  
Best Local Similarity 58.2%; Pred. No. 3.8e-05;  
Matches 103; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1118 GTCTTCAATCATGACCAAGAAATATGAGACCTGGAAGATTTCATTGACTGGCTTTGGG 1177  
DB 598 GTAGCCAGCTGACAGCCACCTCCACGTTGGAGCAGTCTTCTCAACGACTGTTTCAGTG 657  
QY 1178 GAGGCTTTAACTATCATGAGTTCAGTTCATCTTTTCCACGATGCCAGCAAACTTGA 1237  
DB 658 GACACCTTAACTTCCAGATTGAGCACCACCTCTTCCCACCATGCCCGGCACAACTTAC 717  
QY 1238 ACACGTGTTATGCCACTTGTTRAGGAGTTTGCAGCAGCAAAATGTTTACCATACATGG 1294  
DB 718 ACAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCAGG 774

RESULT 9  
US-10-191-513A-6  
;; Sequence 6, Application US/10191513A  
;; Publication No. US20030104596A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abbott Laboratories  
;; APPLICANT: Mukerji, Pardip  
;; APPLICANT: Leonard, Amanda E.  
;; APPLICANT: Huang, Yung-Sheng  
;; APPLICANT: Tapas, Das  
;; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
;; FILE REFERENCE: 6295 US D3  
;; CURRENT APPLICATION NUMBER: US/10/191,513A  
;; CURRENT FILING DATE: 2002-09-25  
;; PRIOR APPLICATION NUMBER: US 09/227,613  
;; PRIOR FILING DATE: 1999-01-08  
;; PRIOR APPLICATION NUMBER: PCT/US98/07422  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: US 08/833,610  
;; PRIOR FILING DATE: 1997-04-11  
;; NUMBER OF SEQ ID NOS: 54  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 1686  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-191-513A-6

Query Match 4.0%; Score 58.6; DB 9; Length 1686;  
Best Local Similarity 58.2%; Pred. No. 4.2e-05;  
Matches 103; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1118 GTCTTCAATCATGACCAAGAAATATGAGACCTGGAAGATTTCATTGACTGGCTTTGGG 1177  
DB 463 GTAGCCAGCTGACAGCCACCTCCACGTTGGAGCAGTCTTCTCAACGACTGTTTCAGTG 522

QY 1178 GAGGCTTTAACTATCATGAGTTCAGTTCATCTTTTCCACGATGCCAGCAAACTTGA 1237  
DB 523 GACACCTTAACTTCCAGATTGAGCACCACCTCTTCCCACCATGCCCGGCACAACTTAC 582  
QY 1238 ACACGTGTTATGCCACTTGTTAAGGAGTTTGCAGCAGCAAAATGTTTACCATACATGG 1294  
DB 583 ACAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCAGG 639

RESULT 10  
US-10-191-513A-7  
;; Sequence 7, Application US/10191513A  
;; Publication No. US20030104596A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abbott Laboratories  
;; APPLICANT: Mukerji, Pardip  
;; APPLICANT: Leonard, Amanda E.  
;; APPLICANT: Huang, Yung-Sheng  
;; APPLICANT: Tapas, Das  
;; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
;; FILE REFERENCE: 6295 US D3  
;; CURRENT APPLICATION NUMBER: US/10/191,513A  
;; CURRENT FILING DATE: 2002-09-25  
;; PRIOR APPLICATION NUMBER: US 09/227,613  
;; PRIOR FILING DATE: 1999-01-08  
;; PRIOR APPLICATION NUMBER: PCT/US98/07422  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: US 08/833,610  
;; PRIOR FILING DATE: 1997-04-11  
;; NUMBER OF SEQ ID NOS: 54  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 7  
;; LENGTH: 1843  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-191-513A-7

Query Match 4.0%; Score 58.6; DB 9; Length 1843;  
Best Local Similarity 58.2%; Pred. No. 4.4e-05;  
Matches 103; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1118 GTCTTCAATCATGACCAAGAAATATGAGACCTGGAAGATTTCATTGACTGGCTTTGGG 1177  
DB 620 GTAGCCAGCTGACAGCCACCTCCACGTTGGAGCAGTCTTCTCAACGACTGTTTCAGTG 679  
QY 1178 GAGGCTTTAACTATCATGAGTTCAGTTCATCTTTTCCACGATGCCAGCAAACTTGA 1237  
DB 680 GACACCTTAACTTCCAGATTGAGCACCACCTCTTCCCACCATGCCCGGCACAACTTAC 739  
QY 1238 ACACGTGTTATGCCACTTGTTAAGGAGTTTGCAGCAGCAAAATGTTTACCATACATGG 1294  
DB 740 ACAAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCAGG 796

RESULT 11  
US-10-191-513A-8  
;; Sequence 8, Application US/10191513A  
;; Publication No. US20030104596A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abbott Laboratories  
;; APPLICANT: Mukerji, Pardip  
;; APPLICANT: Leonard, Amanda E.  
;; APPLICANT: Huang, Yung-Sheng  
;; APPLICANT: Tapas, Das  
;; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
;; FILE REFERENCE: 6295 US D3  
;; CURRENT APPLICATION NUMBER: US/10/191,513A  
;; CURRENT FILING DATE: 2002-09-25  
;; PRIOR APPLICATION NUMBER: US 09/227,613  
;; PRIOR FILING DATE: 1999-01-08  
;; PRIOR APPLICATION NUMBER: PCT/US98/07422  
;; PRIOR FILING DATE: 1998-04-10

;; PRIOR APPLICATION NUMBER: US 08/833,610  
;; PRIOR FILING DATE: 1997-04-11  
;; NUMBER OF SEQ ID NOS: 54  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 8  
;; LENGTH: 2257  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-191-513A-8

Query Match 4.0%; Score 58.6; DB 9; Length 2257;  
Best Local Similarity 58.2%; Pred. No. 5e-05;  
Matches 103; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1118 GTCCTTAATCATGACCAACAAGAAATATGAGACCTGGAGATTTCATTGCTGGCTTTGGG 1177  
DB 1034 CTAGCCAGCTGACAGCCACCTGCAACGTTGGAGCAGTCTCTTCTCAACGACTGGTTCAGTG 1093  
QY 1178 GAGGTCTTAATCATGAGTTCAGACCATCTTTTCCCAACGATGCCAGCACAACACTTGA 1237  
DB 1094 GACACCTTAATCTTCAGATTGAGCACCACCTCTTCCCAACCATGCCCGGCACAACCTTAC 1153  
QY 1238 ACACCTGTTATGCCACTCTTAAAGAGATTGCGACGACAAATGGTTTACCATACATGG 1294  
DB 1154 ACAAGATGCCCGCTGCTGAGTCTCTATGTGCCAAGCATGGCATTAATACCAGG 1210

RESULT 12  
US-09-736-457-355/c  
;; Sequence 355, Application US/09736457  
;; Patent No. US20020168637A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, Tongtong  
;; APPLICANT: Bangur, Chaitanya S.  
;; APPLICANT: Lodes, Michael A.  
;; APPLICANT: Fanger, Gary  
;; APPLICANT: Vedvick, Tom  
;; APPLICANT: Carter, Darrick  
;; APPLICANT: Retter, Marc  
;; APPLICANT: Mannion, Jane  
;; APPLICANT: Fan, Liqun  
;; APPLICANT: Wang, Aljun  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
;; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
;; FILE REFERENCE: 210121.478C15  
;; CURRENT APPLICATION NUMBER: US/09/736.457  
;; CURRENT FILING DATE: 2000-12-13  
;; NUMBER OF SEQ ID NOS: 1864  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 355  
;; LENGTH: 347  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-09-736-457-355

Query Match 3.6%; Score 52; DB 9; Length 347;  
Best Local Similarity 55.6%; Pred. No. 0.00093;  
Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
QY 1133 CCACAAGAAATATGAGACCTGGAGATTTCATTGCTGGCTTTGGGAGGTCTTAACTATC 1192  
DB 340 CCACCTGCAACGTTGGAGCCCTCACTTTTCCAACTAGTGTTCAGCGGCACCTCAACTCC 281  
QY 1193 AGATTGAGCAGCATCTTTTCCCAACGATGCCAGCACAACACTTGAACACTGTTATGCCAC 1252  
DB 280 AGATCGAGCACCCTCTTCCCAAGAGTCCGAGACACAACACTAGCGGGTGGCCCGCC 221  
QY 1253 TTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGTCGACGATTATTTCACAG 1312  
DB 220 TGGTCAAGTCGCTGTGTGCCAAGCAGCGCCTCAGCTACGAGTGAAGCCCTTCCTCACC 161

RESULT 13

US-09-902-941-355/c  
;; Sequence 355, Application US/09902941  
;; Patent No. US20020172952A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Henderson, Robert A.  
;; APPLICANT: Wang, Tongtong  
;; APPLICANT: Watanabe, Yoshihiro  
;; APPLICANT: Johnson, Jeffrey C.  
;; APPLICANT: Retter, Marc W.  
;; APPLICANT: Marnerakis, Margarita  
;; APPLICANT: Carter, Darrick  
;; APPLICANT: Fanger, Gary R.  
;; APPLICANT: Vedvick, Thomas S.  
;; APPLICANT: Bangur, Chaitanya S.  
;; APPLICANT: McNabb, Andria  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
;; FILE REFERENCE: 210121.478C17  
;; CURRENT APPLICATION NUMBER: US/09/902,941  
;; CURRENT FILING DATE: 2001-07-10  
;; NUMBER OF SEQ ID NOS: 2002  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 355  
;; LENGTH: 347  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-902-941-355

Query Match 3.6%; Score 52; DB 9; Length 347;  
Best Local Similarity 55.6%; Pred. No. 0.00093;  
Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
QY 1133 CCACAAGAAATATGAGACCTGGAGATTTCATTGCTGGCTTTGGGAGGTCTTAACTATC 1192  
DB 340 CCACCTGCAACGTTGGAGCCCTCACTTTTCCAACTAGTGTTCAGCGGCACCTCAACTCC 281  
QY 1193 AGATTGAGCAGCATCTTTTCCCAACGATGCCAGCACAACACTTGAACACTGTTATGCCAC 1252  
DB 280 AGATCGAGCACCCTCTTCCCAAGAGTCCGAGACACAACACTAGCGGGTGGCCCGCC 221  
QY 1253 TTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGTCGACGATTATTTCACAG 1312  
DB 220 TGGTCAAGTCGCTGTGTGCCAAGCAGCGCCTCAGCTACGAGTGAAGCCCTTCCTCACC 161

RESULT 14  
US-09-796-692-4558/c  
;; Sequence 4558, Application US/09796692  
;; Publication No. US20020198362A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Mannion, Jane  
;; APPLICANT: Algate, Paul A.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND TI  
;; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
;; FILE REFERENCE: 2077.001200  
;; CURRENT APPLICATION NUMBER: US/09/796,692  
;; CURRENT FILING DATE: 2001-03-01  
;; PRIOR APPLICATION NUMBER: 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: 60/206,201

; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4558
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-4558

Query Match 3.6%; Score 52; DB 9; Length 347;  
Best Local Similarity 55.6%; Pred. No. 0.00093;  
Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY	1133	CCACAAGAATATGACACCTGGAGATTCTATTGACCTGGCTTTGGGAGGTCCTTAACATATC	1192
DB	340	CCACCTGCAACCTGGAGCCCTCACTTTTCCACCAACTGGTTACGGGGCACCTCAACTTCC	281
QY	1193	AGATTGAGCACCATCTTTTCCCAACGATGCCAGACACAACTTGAACACTGTTATGCCAC	1252
DB	280	AGATCGAGCACCACCTCTTTCCCGAGGATGCCGAGACAACTACAGCCGGTGGCCCCGC	221
QY	1253	TTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTGCAGAGTATTATTCACAG	1312
DB	220	TGTCGAAGTCGTGTGTGCCAAGCAGCGCCTCAGCTACGAAGTGAAGCCCTTCTCTACCG	161

RESULT 15  
US-09-849-626-355/c  
; Sequence 355, Application US/09849626  
; Publication No. US20020197669A1  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya  
; APPLICANT: Fanger, Gary  
; APPLICANT: Wang, Aijun  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Switzer, Anne  
; APPLICANT: McNeill, Patricia  
; APPLICANT: Clapper, Jonathan  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.478C16  
; CURRENT APPLICATION NUMBER: US/09/849,626  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 1926  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 355  
; LENGTH: 347  
; TYPE: DNA  
; ORGANISM: Homo sapien
US-09-849-626-355

Query Match 3.6%; Score 52; DB 9; Length 347;  
Best Local Similarity 55.6%; Pred. No. 0.00093;  
Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY	1133	CCACAAGAATATGACACCTGGAGATTCTATTGACCTGGCTTTGGGAGGTCCTTAACATATC	1192
DB	340	CCACCTGCAACCTGGAGCCCTCACTTTTCCACCAACTGGTTACGGGGCACCTCAACTTCC	281
QY	1193	AGATTGAGCACCATCTTTTCCCAACGATGCCAGACACAACTTGAACACTGTTATGCCAC	1252
DB	280	AGATCGAGCACCACCTCTTTCCCGAGGATGCCGAGACAACTACAGCCGGTGGCCCCGC	221
QY	1253	TTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTGCAGAGTATTATTCACAG	1312

Db 220 TGTCGAAGTCGTGTGTGCCAAGCAGCGCCTCAGCTACGAAGTGAAGCCCTTCTCTACCG 161

Search completed: July 2, 2003, 19:28:04  
Job time : 259.306 secs

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 13:22:56 ; Search time 74.2248 Seconds  
(without alignments)  
6036.458 Million cell updates/sec

Title: US-09-857-583-1  
Perfect score: 1461  
Sequence: 1 gaatttcacatctcttg.....tccaaattttacattacc 1461

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 802724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73.8	5.1	1617	2	US-08-834-655-1
2	73.8	5.1	1617	3	US-08-834-033A-1
3	73.8	5.1	1617	3	US-09-363-574-1
4	73.8	5.1	1617	4	US-09-363-526-1
5	73.8	5.1	1617	4	US-09-330-235-17
6	62.4	4.3	449	4	US-09-439-261-38
7	62.4	4.3	449	4	US-09-227-613-37
8	62.4	4.3	473	4	US-09-439-261-37
9	62.4	4.3	473	4	US-09-227-613-36
10	62.4	4.3	655	4	US-09-439-261-3
11	62.4	4.3	655	4	US-09-227-613-3
12	62.4	4.3	864	4	US-09-439-261-12
13	62.4	4.3	864	4	US-09-227-613-13
14	62.4	4.3	1335	4	US-09-439-261-1
15	62.4	4.3	1335	4	US-09-227-613-1
16	58.6	4.0	1686	4	US-09-439-261-6
17	58.6	4.0	1686	4	US-09-227-613-6
18	58.6	4.0	1843	4	US-09-439-261-7
19	58.6	4.0	1843	4	US-09-227-613-7
20	58.6	4.0	2257	4	US-09-439-261-8
21	58.6	4.0	2257	4	US-09-227-613-8
22	50.8	3.5	7218	1	US-08-232-463-14
23	48.6	3.3	1684	2	US-08-831-570-1
24	48.6	3.3	1684	2	US-08-831-575-1
25	48.6	3.3	1685	1	US-08-366-779-4
26	48.6	3.3	1685	1	US-08-789-936-4
27	48.6	3.3	1685	4	US-08-934-254-4

28	38.2	2.6	2220	4	US-09-134-001C-749	Sequence 749, App
c 29	36.8	2.5	1632	4	US-09-134-001C-728	Sequence 728, App
c 30	36.8	2.5	12597	4	US-09-705-299-12	Sequence 12, Appl
31	36.2	2.5	914	4	US-09-475-316A-24	Sequence 24, Appl
32	36.2	2.5	1702	4	US-08-934-254-26	Sequence 26, Appl
c 33	36.2	2.5	3369	2	US-08-619-198-2	Sequence 2, Appl
c 34	36.2	2.5	4170	2	US-08-619-198-4	Sequence 4, Appl
c 35	36.2	2.5	5192	2	US-08-619-198-8	Sequence 8, Appl
c 36	36.2	2.5	5198	2	US-08-619-198-1	Sequence 1, Appl
37	35	2.4	14636	4	US-09-173-914-6	Sequence 6, Appl
38	34.8	2.4	4223	4	US-09-541-782-5	Sequence 5, Appl
39	34.8	2.4	4223	4	US-09-723-820-5	Sequence 5, Appl
c 40	34.4	2.4	991	1	US-08-232-463-19	Sequence 19, Appl
c 41	34.4	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
42	34.2	2.3	244	1	US-08-686-878A-43	Sequence 43, Appl
43	34.2	2.3	1224	4	US-09-134-001C-562	Sequence 562, App
44	34	2.3	4330	3	US-09-310-293-1	Sequence 1, Appl
45	34	2.3	4330	4	US-09-579-376-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-834-655-1  
; Sequence 1, Application US/08834655  
; Patent No. 5968809  
; GENERAL INFORMATION:  
; APPLICANT: KNUITZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834.655  
FILING DATE: 11-APR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RAE-VENTER, BARBARA  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: CGNE.124.0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 328-4400  
TELEFAX: (650) 328-4477  
TELEX: N/A

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1617 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-834-655-1

Query Match 5.1%; Score 73.8; DB 2; Length 1617;  
Best Local Similarity 47.5%; Pred. No. 1.1e-11;  
Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;



QY 1068 TTCAGTGGAGAGTTGTCATTCGAGCTCGACATCATCTCAAAATACGCTTGTCTTCAAAAT 1127  
DB 1129 CGGTATGCCGTGATCTCGAGGAGGAGGCGGTCGATATGATTTCTTACGAAGCAGAT 1188  
QY 1128 CATGACCACAAGAAATATGAGACCTGGAAGATTCAATGACTGGCTTTGGGGAGGTCTTAA 1187  
DB 1189 CATCAGGGTCTGATGTCACCCGGTCTATTTGCCAACTGGTTACGGGTGGATTGAA 1248  
QY 1188 CTATCAGATTGACACATCTTTTCCCAAGATGCGACGACACAACTTGAACACTGTTAT 1247  
DB 1249 CTATCAGATCGAGCACCACCTTGTTCCTTCGATGCTCGCCACAACTTTTCAAGATCCA 1308  
QY 1248 GCCACTTGTAAAG 1260  
DB 1309 GCCTGCTGCGAG 1321

## RESULT 3

US-09-363-574-1  
; Sequence 1, Application US/09363574  
; Patent No. 6136574  
; GENERAL INFORMATION:  
; APPLICANT: KNUTZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
; STREET: 2001 FERRY BUILDING  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/363,574  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WARD, MICHAEL R.  
; REGISTRATION NUMBER: 38,651  
; REFERENCE/DOCKET NUMBER: CGAB-202 USA  
; TELEPHONE: (415) 433-4150  
; TELEFAX: (415) 433-8716  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1617 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; US-09-363-574-1

Query Match 5.1%; Score 73.8; DB 3; Length 1617;  
Best Local Similarity 47.5%; Pred. No. 1.1e-11;  
Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;  
QY 500 TTCAATCAGCTATCTTAATGGAGTTGCGTGGCAACAATGGGATGGTTAATCCATGAAT 559  
DB 531 TGTCTCGGCTGCGCTTTTGGTCTCTTCTGGCAGCAGTCCGATGGTTGGCTCAGACT 590  
QY 560 TCGCACATCATCTGTTTCAAAAACAGATACTACAAATGATTTGGCCAGCTATTTCTGTTG 619

DB 591 TTTTGCATCAGAGGCTTTCAGGACCGTTTTCGGGGGATCTTTTCGGGCCCTCTCTTGG 650  
QY 620 GAAACATTTTACAGGATCTCATCTGCTGTTGGTAAAGAGCAGCAACAATGTGCAATCAG 679  
DB 651 GAGGTGCTGCCAGGGCTTCTCGTCTCGTGGTGAAGGACAAGCACAACACTCACCACG 710  
QY 680 CAGCCACAATGTTGTTGGAGAGCAGGAGATCTTGAATTTAGTCCCATCTTATGCTACAG 739  
DB 711 CCGCCCAACAGTCCAGCGGAGGATCCCGACATTTGA--CACCCACCCCTCTGTTGACCTG 768  
QY 740 TGCAGAACATCTCAACAATTTATCTCAGGATTCATGSGTTATGACTCTATTCAGATGGC 799  
DB 769 GAGTGAGCATGCGTTGGAGATGTTCTCGGATGTCAGATGAGGAGCTGACCCCATGTG 828  
QY 800 AACATGTTCAATGGACATTT-----CATGTTACCATTTCTCCCG 836  
DB 829 GTCGCGTTTCATGCTCTGAACAGACCTGTTTACTTCCCATTTCTCGTTTGGCCG 888  
QY 837 TCTCTGCTGCTTCTTCAGTCAATCATTTTGTGTTAGTCAGATGCCAACTCATTTATTTATGA 896  
DB 889 TCTCTGCTGCTGCTCCAGTCCATTTCTTTGTGCTGCTTAACGGTCCAGGCCACAAGCC 948  
QY 897 CTATTACAGAAAT-----ACTGCGATTTATGAACAGGTTGGTCTCTCTTTGCACTGGGC 950  
DB 949 CTCGGGGCGCGTGTGCCCATCTCGTTGGTCGAGCAGCTGTCGCTTGGATGCACTGGAC 1008  
QY 951 TTGTCATTTGGTCAATTTGT---ATTTCCTACCCGATTTGGTCAACTAGAATAATGTTCTT 1007  
DB 1009 CTGCTACCTCGCCACCATGTTCTGTTTCAATCAAGGATCCCGTCAACATGCTGGTACTT 1068  
QY 1008 CTTGTTTCTCATCTTTGTTGAGGTTTCTCTGCTCTCTCATGTAGTTACTTTCAATCATTA 1067  
DB 1069 TTTGGTGTGTCGAGCGGTGTGCGGAAACTTTTGGCGATGCTGTCTCGCTCAACACCAA 1128  
QY 1068 TTCAGTGGAGAGTTTGCATTTGAGCTCGAACATCATCTCAAAATACCTTGTCTCTTCAAT 1127  
DB 1129 CGGTATGCCGTGATCTCGAAGGAGGCGGTCGATATGGATTTCTCAGGAAGCAGAT 1188  
QY 1128 CATGACCACAAGAAATATGAGACCTGGAAGATTCATTTGAGTGGCTTTGGGAGGTCTTAA 1187  
DB 1189 CATCAGGGTCTGATGTCACCCGGTCTATTTGCCAACTGTTTACGGGTGGATTGAA 1248  
QY 1188 CTATCAGATTGACACATCTTTTCCCAAGATGCGCAGCACAACCTTGAACACTGTTAT 1247  
DB 1249 CTATCAGATCGAGCACCACCTTGTTCCTTCGATGCTGCGCACAACTTTTCAAGATCCA 1308  
QY 1248 GCCACTTGTAAAG 1260  
DB 1309 GCCTGCTGCGAG 1321

## RESULT 4

US-09-363-526-1  
; Sequence 1, Application US/09363526  
; Patent No. 6410288  
; GENERAL INFORMATION:  
; APPLICANT: KNUTZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
; STREET: 2001 FERRY BUILDING  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363.526  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-201 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1617 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-09-363-526-1

Query Match 5.1%; Score 73.8; DB 4; Length 1617;

Best Local Similarity 47.5%; Pred. No. 1.1e-11;  
Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;

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QY 500 TTCCATCAGCTATTCTAATGGGAGTTCGGTGGCAACAATGGGATGGTTAATCCATGAAT 559
DB 531 TGCTCTCGGCTGGCGCTTTGGGCTGTCTGGCAGCAGTGGCGATGGTTGGCTCAGCACT 590
QY 560 TCGCACATCATGATGTTTCAAAAACAGATACTACAATGATTTGGCCAGCTATTTCGTTG 619
DB 591 TTTTGATCACCAGGCTCTCCAGGACCGTTTCTGGGTGATCTTTTCCGGCCCTTCITGG 650
QY 620 GAAACTTTTACAAGGATTTCTCATCTGTGTGGTGGAAAGAGCAGACACAATGTGCATCAG 679
DB 651 GAGGTGTCTGCCAGGGCTTCTCGTCTCGTGGTGGAGGACAAAGCAACACTCACCACG 710
QY 680 CAGCCACAATGTTGTTGGAGGAGCAGGATCTTGAATTTAGTCCCATCTCTATGCTACAG 739
DB 711 CCGCCCCAAGCTCCAGCGGAGGATCCGACATGTA--CACCCACCTCTGTGTGACCTG 768
QY 740 TGGCAGAACATCTCAACAATTTATCTCAGGATTCATGGGTTATGACTCTATTCAGATGCG 799
DB 769 GAGTGAGCATGCGTTGGAGATGTTCTCGGATGTCCAGATGAGGAGCTGACCCGATGTG 828
QY 800 AACATGTTTCATTGGACATTT-----CATGTTACCATTTCTCTCCG 836
DB 829 GTCCGGTTTCATGCTCTGCTGAACACAGCTGCTGTTTACTTCCCATTTCTCTGTTGCCG 888
QY 837 TCTCTCGTGGCTTCTCAGTCAATCTTTTGTAGTCAGATGCCAATCTATTTATGA 896
DB 889 TCTCTCTGTGCTCCAGTCCATCTTTTGTGCTGCTTAACGCTCAGGCCCAAGCC 948
QY 897 CTATTACAGAAAT-----ACTGCGATTTATGAACAGTTGGTCTCTCTTTTGCATCGGC 950
DB 949 CTCGGCGCGCGTGTGCCCATCTCTGTTGGTCGAGCAGCTGTCGTTGGATGCATGGAC 1008
QY 951 TTGGTCAATGGTCAAAATGT---ATTTCTACCCGATTTGGTCAACTAGATAATGTTCTT 1007
DB 1009 CTGGTACCTGCCACCATGTTGCCATCTCTGTTGGTGGAGCAGCTGTCGCTTGGCATTC 1068
QY 1008 CCTGTTTCTCATCTTGTGAGCTTCCCTCTCTCATCTAGTACTTACTTCAATCATTA 1067
DB 1069 TTTGGTGTGCGAGCGGTGTCGGAATCTTGTGGGATGCTGTTCTGCTGCTCAACCAAA 1128
QY 1068 TTCAATGAGGAAGTTTGCATTTGAGCTCGAACATCATGTCAAAATACGCTTCTCTCAAT 1127
DB 1129 CGGTATCCCTGTATCTCGAAGGAGGAGCGGTGATGATGATTTCTTCACGAAGCAGAT 1188
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QY 1128 CATGACCACAGAAATATGAGACCTGGAGGATTCATTGACTGGCTTTGGGAGGCTTAA 1187
DB 1189 CATCAGGGTCTGATGTCACCGGGGTCTATTGCCAATCTGGTTCACGGGTGGATTGNA 1248
QY 1188 CTATCAGATTGAGCACCATTCTTTCCCAACGATGCCAGACACAACACTTGAACACTGTTAT 1247
DB 1249 CTATCAGATCGAGCACCATTGTTCCCTTCGATGCTGCCACAACTTTTCAAGATGCA 1308
QY 1248 GCCACTGTTTAAG 1260
DB 1309 GCCTGCTGTCGAG 1321
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## RESULT 5

US-09-330-235-17

Sequence 17, Application US/09330235  
Patent No. 6459018  
GENERAL INFORMATION:  
APPLICANT: Knutzon, Debbie  
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS  
FILE REFERENCE: MOCO.156.0005  
CURRENT APPLICATION NUMBER: US/09/330,235  
CURRENT FILING DATE: 1999-06-10  
PRIOR APPLICATION NUMBER: 60/089,043  
PRIOR FILING DATE: 1998-06-12  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 17  
LENGTH: 1617  
TYPE: DNA  
ORGANISM: Mortierella alpina  
US-09-330-235-17

Query Match 5.1%; Score 73.8; DB 4; Length 1617;  
Best Local Similarity 47.5%; Pred. No. 1.1e-11;  
Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;

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QY 500 TTCCATCAGCTATTCTAATGGGAGTTCGGTGGCAACAATGGGATGGTTAATCCATGAAT 559
DB 531 TGCTCTCGGCTGGCGCTTTTGGGCTGTCTTCTGGCAGCAGTGGCGATGGTTCAGCACT 590
QY 560 TCGCACATCATGATGTTTCAAAAACAGATACTACAATGATTTGGCCAGCTATTTCGTTG 619
DB 591 TTTTGATCACCAGGCTCTCCAGGACCGTTTCCAGGAGCTTTTGGGTGATCTTTTCCGGCCCTTCITGG 650
QY 620 GAAACTTTTACAAGGATTTCTCATCTGTGTGGTGGAAAGAGCAGACACAATGTGCATCAG 679
DB 651 GAGGTGTCTGCCAGGGCTTCTCGTCTCGTGGTGGAGGACAAAGCAACACTCACCACG 710
QY 680 CAGCCACAATGTTGTTGGAGGAGCAGGATCTTGAATTTAGTCCCATCTCTATGCTACAG 739
DB 711 CCGCCCCAAGCTCCAGCGGAGGATCCGACATGTA--CACCCACCTCTGTGTGACCTG 768
QY 740 TGGCAGAACATCTCAACAATTTATCTCAGGATTCATGGGTTATGACTCTATTCAGATGCG 799
DB 769 GAGTGAGCATGCGTTGGAGATGTTCTCGGATGTCCAGATGAGGAGCTGACCCGATGTG 828
QY 800 AACATGTTTCATTGGACATTT-----CATGTTACCATTTCTCTCCG 836
DB 829 GTCCGGTTTCATGCTCTGCTGAACACAGCTGCTGTTTACTTCCCATTTCTCTGTTGCCG 888
QY 837 TCTCTCGTGGCTTCTCAGTCAATCTTTTGTAGTCAGATGCCAATCTATTTATGA 896
DB 889 TCTCTCTGTGCTCCAGTCCATCTTTTGTGCTGCTTAACGCTCAGGCCCAAGCC 948
QY 897 CTATTACAGAAAT-----ACTGCGATTTATGAACAGTTGGTCTCTCTTTTGCATCGGC 950
DB 949 CTCGGCGCGCGTGTGCCCATCTCTGTTGGTCGAGCAGCTGTCGTTGGATGCATGGAC 1008
QY 951 TTGGTCAATGGTCAAAATGT---ATTTCTACCCGATTTGGTCAACTAGATAATGTTCTT 1007
DB 1009 CTGGTACCTGCCACCATGTTGCCATCTCTGTTGGTGGAGCAGCTGTCGCTTGGCATTC 1068
QY 1008 CCTGTTTCTCATCTTGTGAGCTTCCCTCTCTCATCTAGTACTTACTTCAATCATTA 1067
DB 1069 TTTGGTGTGCGAGCGGTGTCGGAATCTTGTGGGATGCTGTTCTGCTGCTCAACCAAA 1128
QY 1068 TTCAATGAGGAAGTTTGCATTTGAGCTCGAACATCATGTCAAAATACGCTTCTCTCAAT 1127
DB 1129 CGGTATCCCTGTATCTCGAAGGAGGAGCGGTGATGATGATTTCTTCACGAAGCAGAT 1188
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QY 1008 CCTGTTCTCATCTTGTGGAGGTTTCCTGCTCTCTCATGTAGTTACTTTCATCATTA 1067
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Db 1069 TTTGGTTCGACGGCGGTGTCGGAACATTTGTTGGCGATGCTGTTCTCGCTCAACACAA 1128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1068 TTCAGTGGAGAAGTTTGCATTTGAGCTCGAACATCATGTCAAATAGCTTGTCTTCAAAT 1127
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1129 CGGTATGCTGTGATCTCGAAGGAGGCGGTGCGATAGTATTTCTCAGGAGCAGAT 1188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1128 CATGACCACAAGAAATATGAGACCTGGAAGATTATGACTGCTTGGGGAGGTCTTAA 1187
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Db 1189 CATCAGGGTGTGTGATGTCACCCGGGTCTATTTGCCAACTGTTACGGGTGGAUTGAA 1248
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QY 1188 CTATCAGATTGACCACTCTTTTCCCAAGCATGCGACGACACAACTTGNACACTGTTAT 1247
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Db 1249 CTATCAGATTGACCACTCTTTTCCCTCGATGCTCGCCCAACATTTTTCAAAGATCCA 1308
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QY 1248 GCCACTTGTAAAG 1260
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Db 1309 GCCTGCTGTCGAG 1321
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RESULT 6

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US-09-439-261-37
; Sequence 38, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: k = g or t/u at position 5
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: m = a or c at position 6
US-09-439-261-37

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Query Match 4.3%; Score 62.4; DB 4; Length 449;
Best Local Similarity 59.7%; Pred. No. 1.2e-08;
Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTCATTCAGCTGGCTTTGGGAGGT 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 CAGCTCCAGGCCACATGCNATGCCAAAGTCTGCCCTTCAATGACTGGTTCAGTGGACAC 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1183 CTTAACTATCAGATTGAGCACCACCTTTTCCCAAGCATGCCACGACACAACTTGAACACT 1242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 CTCACCTCCAGATTGAGCACCACCTTTTCCCAAGCATGCCCTCGACACAAATTACCACAAA 301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1243 GTTATGCCACTTGTGAAGAGTTTGCAGCAGCAAAATGTTTACCATATACATGTCGA 1298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 GTGGCTCCCTGGTCAGTCCTTGTGTGCCAAGCATGGCATAGAGTACCAGTCCAA 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 7

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US-09-227-613-37
; Sequence 37, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-613-37

Query Match 4.3%; Score 62.4; DB 4; Length 449;
Best Local Similarity 59.7%; Pred. No. 1.2e-08;
Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTCATTCAGCTTTGGGAGGT 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 8

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US-09-439-261-37
; Sequence 37, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-37

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Query Match 4.3%; Score 62.4; DB 4; Length 473;
Best Local Similarity 59.7%; Pred. No. 1.2e-08;
Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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RESULT 14  
US-09-439-261-1  
; Sequence 1, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:

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QY 1243 GTATGCCACTTGTTAAGGAGTTTCAGCAGCAAAATGGTTTACCATACATGCTCGA 1298  
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Search completed: July 2, 2003, 16:51:55  
Job time : 79.2248 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 12:59:11 ; Search time 3851.68 Seconds  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
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- 5: gb.pat.\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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2	1344	92.0	1344	3	AF078796 Caenorhab
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4	658.2	45.1	38060	3	CET13F2 Z81122 Caenorhabd
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21	82.4	5.6	2012	8	PPA22980 Physcomit
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ALIGNMENTS

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LOCUS  
DEFINITION  
Caenorhabditis elegans delta5-fatty acid desaturase (fat-4) mRNA,  
complete cds.  
ACCESSION  
AF114440  
VERSION  
AF114440.1 GI:4235625  
SOURCE  
Caenorhabditis elegans.  
ORGANISM  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE  
1 (bases 1 to 1461)  
AUTHORS  
Watts,J.L. and Browse,J.  
TITLE  
Isolation and characterization of a Delta 5-fatty acid desaturase

JOURNAL from Caenorhabditis elegans  
MEDLINE Arch. Biochem. Biophys. 362 (1), 175-182 (1999)  
PUBMED 9917288  
9917342  
REFERENCE 2 (bases 1 to 1461)  
AUTHORS Watts, J.L. and Browse, J.  
TITLE Direct Submission  
JOURNAL Submitted (16-DEC-1998) Institute of Biological Chemistry,  
Washington State University, Clark Hall, Pullman, WA 99164-6340,  
USA

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LOCUS  
DEFINITION Caenorhabditis elegans delta 5 fatty acid desaturase (des-5) mRNA,  
complete cds.  
ACCESSION AF078796  
1344 bp mRNA linear INV 11-DEC-1998

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AF078796.1 GI:4003522
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoides; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 1344)
Michaelson, L.V., Napier, J.A., Lewis, M., Griffiths, G., Lazarus, C.M.
and Stobart, A.K.
Functional identification of a fatty acid desaturase gene
from Caenorhabditis elegans
FEBS Lett. 439 (3), 215-218 (1998)
95059458
9845325
2 (bases 1 to 1344)
Michaelson, L.V., Napier, J.A., Lazarus, C.M., Griffiths, G. and
Stobart, A.K.
Direct Submission
Submitted (16-JUL-1998) Biological Sciences, University of Bristol,
Woodland Road, Bristol BS8 1UG, UK
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DEFINITION Sequence 2 from Patent WO9933958.

AX020906 1344 bp DNA linear PAT 07-SEP-2000

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VERSION AX020906.1 GI:10044591
KEYWORDS
SOURCE
ORGANISM
REFERENCE
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Desaturase
Patent: WO 9933958-A 2 08-JUL-1999;
MICHAELSON LOUISE (GB); STOBART KEITH (GB); UNIV BRISTOL (GB);
NAPIER JOHNATHAN A (GB)
JOURNAL
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823 TTACCAATTCCTCCGTCCTCTCGTGGCTCTTTCAGTCAATCATTTTGTGTTAGTCAGATGCCA 882

781 TTACCAATTCCTCCGTCCTCTCGTGGCTCTTTCAGTCAATCATTTTGTGTTAGTCAGATGCCA 840

883 ACTCATATTATGACTATTACAGAATACTCGGATTATGAACAGTTCGCTCTCTCTTTG 942

841 ACTCATATTATGACTATTACAGAATACTCGGATTATGAACAGTTCGCTCTCTCTTTG 900

943 CACTGGGCTTGGTCAATTTGGGCAATTTATTTCTACCGGATTTGGTCAACTAGAATAATG 1002

901 CACTGGGCTTGGTCAATTTGGGCAATTTATTTCTACCGGATTTGGTCAACTAGAATAATG 960

1003 TCTTCTCTTGTTCATCTCTGAGGTTTCTGCTCTCTCATGATGATTTACTTTCAAT 1062

961 TCTTCTCTTGTTCATCTCTGAGGTTTCTGCTCTCTCATGATGATTTACTTTCAAT 1020

1063 CATTTATTCAGTGGAGAAATTTGCAATGAGCTCGAATCATCTGCAAAATACGCTTCTCTT 1122

1021 CATTTATTCAGTGGAGAAATTTGCAATGAGCTCGAATCATCTGCAAAATACGCTTCTCTT 1080

1123 CAAATCATGACCAACAAGAAATATGAGACCTGGAAGATTCATTTGCTGCTTTGGGAGGT 1182

1081 CAAATCATGACCAACAAGAAATATGAGACCTGGAAGATTCATTTGCTGCTTTGGGAGGT 1140

1183 CTTAACTATCAGATTTGAGCACCATCTTTTCCCAAGATGCCAGACACAACTTGAACACT 1242

1141 CTTAACTATCAGATTTGAGCACCATCTTTTCCCAAGATGCCAGACACAACTTGAACACT 1200

1243 GTTATGCCACTTTGTTAAGGAGTTTGCAGCAGCAAAATGTTTACCATACATGTTGCGACGAT 1302

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1303 TATTTACAGAGATTTGCTGCTTGAATTTGAGCAATTTCCGAAATATTGCAAAATGTTGCTGT 1362

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1363 AAATTTGACTAAAAAGATTGCCTAG 1386

1321 AAATTTGACTAAAAAGATTGCCTAG 1344

RESULT 4

CE113F2 38060 bp DNA linear INV 11-DEC-2001

LOCUS Caenorhabditis elegans cosmid T13F2, complete sequence.

DEFINITION 281122

ACCESSION 281122

VERSION 281122.1 GI:1628203

KEYWORDS HTG; Caveolin; Cyclin D; Cytochrome B5; Human KIAA0170 protein; Major Sperm Protein; Single-stranded DNA binding protein P9.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1

REFERENCE none.

AUTHORS

TITLE Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium

JOURNAL Science 282 (5396), 2012-2018 (1998)

MEDLINE 99059613

PUBMED 9851916

REMARK The C.elegans Sequencing Consortium.

2 (bases 1 to 38060)

AUTHORS Swinburne, J.

TITLE Direct Submission

JOURNAL Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jesus@anger.ac.uk or rw@nematode.wustl.edu

COMMENT Coding sequences below are predicted from computer analysis, using predictions from GeneFinder (P. Green, D. Washington), and other available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis see: <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Tl3f2>

**IMPORTANT:** This sequence is not the entire insert of clone Tl3F2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone Tl3F2 is at 1 in this sequence. The true left end of clone W0802 is at 37953 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence AL022473. The end of this sequence (37953..38060) overlaps with the start of sequence Z70271.

**IMPORTANT:** This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

## FEATURES

source

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/db\_xref="taxon:6239"

/chromosome="IV"

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4956..5339

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comes from this gene

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comes from this gene

cDNA EST YK62F1.3 comes from this gene; cDNA EST YK64E1.3  
comes from this gene

cDNA EST YK74B2.3 comes from this gene; cDNA EST YK78G5.3  
comes from this gene

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cDNA EST YK106H8.3 comes from this gene; cDNA EST  
YK112G9.3 comes from this gene

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Matches 924; Conservative 0; Mismatches 13; Indels 218; Gaps 4;

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Qy	620	GAACATTTTACAA-----	633
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Db	35689	CCCATTCATCTCAGTGGGAGACATCTCAACAATTTCTCAGGATTCATGGTTAT	35748
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RESULT 5	AF031477	1463 bp	mRNA	linear	INV 02-MAY-1998
LOCUS	AF031477				
DEFINITION	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.				
ACCESSION	AF031477	GI:3088519			
VERSION	AF031477.1				
KEYWORDS	Caenorhabditis elegans.				
SOURCE	Caenorhabditis elegans.				
ORGANISM	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.				
REFERENCE	1 (bases 1 to 1463)				
AUTHORS	Sayanova, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G., Christie, W.W., Shewry, P.R. and Napier, J.A.				
TITLE	Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)				
MEDLINE	97268723				
PUBMED	9108131				
REFERENCE	2 (bases 1 to 1463)				
AUTHORS	Napier, J.A., Hey, S.J., Lacey, D.J. and Shewry, P.R.				
TITLE	Identification of a Caenorhabditis elegans Delta6-fatty-acid-desaturase by heterologous expression in Saccharomyces cerevisiae				
JOURNAL	Biochem. J. 330 (Pt 2), 611-614 (1998)				
MEDLINE	98149727				
PUBMED	9480865				
REFERENCE	3 (bases 1 to 1463)				
AUTHORS	Napier, J.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-OCT-1997) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK				



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Qy	793	AGATGGCAACATGTTCTATTGGACATTTATGTTACATCTCCCTGCTCTCTGCTGGCTCTT 852
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Qy	913	CGGATTTATGAACAGGTTGGTCTCTCTTTGACATGGGCTTGGTCAATGGGTCATTTGAT 972
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Qy	1333	CAATTCGCAATATTTGC 1349
Db	1298	CAATGAAAATATGGC 1314

RESULT 7	
CEW08D2	
LOCUS	CEW08D2 30748 bp DNA linear INV 24-JAN-2002
DEFINITION	Caenorhabditis elegans cosmid W08D2, complete sequence.
ACCESSION	Z70271
VERSION	Z70271.1 GI:1236102
KEYWORDS	Htc; Collagen; human myeloid cell line protein like; Transporter
SOURCE	Caenorhabditis elegans.
ORGANISM	Caenorhabditis elegans
REFERENCE	1 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS	none.
TITLE	Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium
JOURNAL	Science 282 (5396), 2012-2018 (1998)
MEDLINE	99069613
PUBMED	9851916
REMARK	The C.elegans Sequencing Consortium.
REFERENCE	2 (bases 1 to 30748)
AUTHORS	Swinburne,J. and Alnscough,R.
TITLE	Direct Submission
JOURNAL	Submitted (23-MAR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematoe.wustl.edu
COMMENT	Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information. Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is not the entire insert of clone W08D2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone W08D2 is at 1 in this sequence. The true right end of clone W08D2 is at 5560 in sequence Z70284. The true left end of clone K07F5 is at 30645 in this sequence. The end of this sequence (1..108) overlaps with the end of sequence Z81122. The end of this sequence (30645..30748) overlaps with the start of sequence Z70284.

960307: Dual-authors: June Swinburne & Rachael Ainscough For a graphical representation of this sequence and its analysis see: <http://www.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=W08D2>

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

#### FEATURES

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620 GAAACTTTTACAAGATTCTCATCTGGTGGTGTGGAACAGCAGACAATGTGCATCAG 679  
Db GAGGTCTGCCAGGCTTCTCGTCTCATGTTGGGAAGCACAAGACAACATCACCAG 640  
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Best Local Similarity 48.0%; Pred. No. 3.3e-11;
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ACCESSION AJ250735
VERSION AJ250735.1 GI:8670978
KEYWORDS cytochrome b5; delta 6-fatty acid desaturase; desaturase.
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ORGANISM Ceratodon purpureus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditracheae; Ceratodon.
REFERENCE 1 (bases 1 to 2160)
AUTHORS Sperling, P., Lee, M., Girke, T., Zahringer, U., Stymne, S. and Heinz, E.
TITLE A bifunctional delta-fatty acyl acetylase/desaturase from the
moss Ceratodon purpureus. A new member of the cytochrome b5
superfamily
JOURNAL Eur. J. Biochem. 267 (12), 3801-3811 (2000)
MEDLINE 20307617
PUBMED 10848999
REFERENCE 2 (bases 1 to 2160)
AUTHORS Sperling, P.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1999) Sperling P., Dept. Plant Physiology,
Institut fuer Allgemeine Botanik, Universitaet Hamburg,
Ohnhorststrasse 18, D-22609 Hamburg, GERMANY
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Best Local Similarity 48.0%; Pred. No. 3.3e-11;
Matches 369; Conservative 0; Mismatches 384; Indels 15; Gaps 3;

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Qy 738 AGTGCCAGAACATCTCAACAATTTATCTCAGAGATTCACTGGGTTATGACTCTATTTCAGATG 797
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SOURCE Mortierella alpina.  
ORGANISM Mortierella alpina  
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;  
Mortierellaceae; Mortierella.  
REFERENCE 1 (bases 1 to 1374)  
AUTHORS Xing,L., Li,M., Liu,L., Hu,G. and Zhang,L.  
TITLE Expression of Mortierella alpina delta 6-fatty acid desaturase gene in Saccharomyces cerevisiae  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1374)  
AUTHORS Xing,L., Li,M., Liu,L., Hu,G. and Zhang,L.  
TITLE Direct Submission  
JOURNAL Submitted (26-SEP-2000) Department of Microbiology, Nankai University, 94 Weijin Road, Tianjin 300071, P.R. China  
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Query Match 6.1%; Score 89.2; DB 8; Length 1374;  
Best Local Similarity 48.4%; Pred. No. 3.6e-10;  
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## ORIGIN

Query Match 6.1%; Score 89.2; DB 8; Length 1374;  
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QY 505 TCAGCTATTCTAATGGAGTGGTGGCAACAATTTGGGATGTTAATCCATGAATTCGCA 564  
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## RESULT 15

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 DEFINITION AF465283  
 ACCESSION AF465283.1 GI:18483178  
 VERSION  
 KEYWORDS Mortierella alpina.  
 SOURCE Mortierella alpina  
 ORGANISM

Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae; Mortierella.  
 1 (bases 1 to 1947)  
 AUTHORS Liu, L., Li, M., Hu, G. and Xing, L.  
 TITLE Cloning and sequence analysis of the delta 6 fatty acid desaturase gene from Mortierella alpina ATCC16266 genomic and cDNA Unpublished  
 JOURNAL 2 (bases 1 to 1947)  
 REFERENCE Xing, L., Liu, L., Li, M. and Hu, G.  
 AUTHORS Direct Submission  
 TITLE Submitted (04-JAN-2002) Microbiology, Naikai University, Weijing road 94th, Tianjin 300071, China  
 JOURNAL Location/Qualifiers  
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BASE COUNT 384 a 536 c 504 g 523 t  
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Query Match 6.1%; Score 89.2; DB 8; Length 1947;  
 Best Local Similarity 48.4%; Pred. No. 3.5e-10;  
 Matches 396; Conservative 0; Mismatches 388; Indels 34; Gaps 4;

QY 505 TCAGCTATTCTAATGGAGTGGTGGCAACAATTTGGGATGTTAATCCATGAATTCGCA 564  
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QY 565 CATCATCAGTTGTTCAAAAACAGATACATACTAATGATTGGCCAGCTATTTCGTGGAAAC 624  
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Job time : 3865.68 secs



DR WPI; 2000-431293/37.  
 XX P-PSDB; AAY96721.  
 XX Purified protein having desaturase activity, useful for creating a  
 PT double-bond between two carbons  
 XX  
 XX Claim 6; Fig 6B; 74pp; English.  
 CC This cDNA encodes Caenorhabditis elegans fatty acid delta-5 desaturase.  
 CC The cDNA was isolated from cosmid Wf13f2 and the gene, designated Fat-4.  
 CC The sequence is useful for recombinant production of the enzyme and for  
 CC generating transformed host cells and transgenic plants. The desaturase  
 CC can be used for creating a double-bond between two carbons. In  
 CC particular, the enzyme is useful for producing polyunsaturated fatty  
 CC acids and for generating enzyme-specific antibodies useful for  
 CC identifying desaturases. Oil-seed plants may be engineered to incorporate  
 CC the enzyme, so that the plants produce seed oil rich in fatty acids. The  
 CC fatty acids could be incorporated usefully into infant formula, foods of  
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 XX  
 XX Sequence 1461 BP; 426 A; 292 C; 273 G; 470 T; 0 other;  
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Query Match 100.0%; Score 1461; DB 21; Length 1461;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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 AC AAX8961;  
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 DT 24-SEP-1999 (first entry)  
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 DE C. elegans delta 5-fatty acid desaturase encoding cDNA.  
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 KW Delta 5-fatty acid desaturase; dihomogamma linolenic acid; gene therapy;  
 KW arachidonic acid; cholesterol; polyunsaturated fatty acid; foodstuff;  
 KW dietary supplement; prostaglandin; ss.  
 OS Caenorhabditis elegans.  
 XX  
 PN WO9933958-A2.  
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08-JUL-1999.

23-DEC-1998; 98WO-GB03895.

29-JUN-1998; 98GB-0014034.

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[illegible]

Michaelson L, Napier JA, Stobart K;

WPI; 1999-444067/37.

P-PSDB; AAY21890.

## New isolated delta5-fatty acid desaturase enzymes useful in gene therapy

Claim 4; Page 21; 36pp; English.

The invention provides delta 5-fatty acid desaturases obtained from *Morone saxatilis* and *Caenorhabditis elegans*. The Delta 5-fatty acid desaturases catalyze the production of polyunsaturated fatty acids, e.g. the conversion of dihomogamma linolenic acid to arachidonic acid. The genes can be used in gene therapy as a preventative treatment, e.g. in patients suffering from high levels of cholesterol or other conditions where administration of polyunsaturated fatty acids may have beneficial disease-preventative effects. The polyunsaturated fatty acids can be used in foodstuffs or dietary supplements. The Delta 5-fatty acid desaturases can also be used for the synthesis of prostaglandins or modulation of the synthesis. The products can also be used for detection and diagnosis. The present sequence represents the cDNA encoding the *C. elegans* delta 5-fatty acid desaturase.

Sequence 1344 BP; 396 A; 269 C; 261 G; 418 T; 0 other;

Query Match	92.0%;	Score 1344;	DB 20;	Length 1344;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 1344;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

43 ATGGTATTACGAGAGCAAGAGCATGAGCCATTCTTCATTAAATATGATGGAAATGGTGT 102

1 ATGGTATTACGAGAGCAAGAGCATGAGCCATTCTTCATTAAAAATTGATGGAAAAATGGTGT 60

103 CAAATTGACGATGCTGTCCTGAGATCACATCCAGGTGGTAGTGCAATTACTACCTATAAA 162

61 CAAATTGACGATGCTGTCTGAGATCACATCCAGGTGGTAGTGCAATTACTACCTATAA 120

163 AATGGATGCCACTACCGTATTCCACACATTCCTGGTTCTAAAGAAGCGTATCAA 222

121 AATATGGATGCCACTACCGTATTCACACATTCCTAAAGACGGTATCAA 180

223 TGGCTGACAGAAATTGAAAAAGAGTGCCCTACACAAGAACCAGAGATCCCAGATATTAAAG 282

181 TGGCTGACAGAAATTGAAAAGAGTGCCCTACACAAGAACCCAGAGATCCCAGATATTAAAG 240

283 GATGACCCAATCAAAGGAATTGATGATGTGAACATGGGAACCTTCAATATTTCTGAGAAA 342

241 GATGACCCAATCAAAGGAATTGATGATGTGAACATGGGAACTTTCAATATTTCTGAGAAA 300

343 CGATCTGCCCAATAAAAGTTTCACCTGATCTACGTATGCGAGTTCGTGCAGAAGGA 402

301 CGATCTGCCCAATAAAAGTTTCACTGATCTACGTATGCGAGTTCGTGCAGAAGGA 360

403 CTTATGGATGGATCTCCTTTTGTTCTACATTAGAAAAATTCTTGAAACAATCTTCACAATT 462

361 CTTATGGATGGATCTCCTTTGTTCTACATTAGAAAAATTCTTGAAACAAATCTTCACAAATT 420

463 CTTTTCATCTACCTTCAATACCAACACATATATCTCCATCAGCTATTCTAATGGGA 522

421 CTTTTCATCTACCTTCAATACCACACATATTATCTTCCATCAGCTATTCTAATGGGA 480

523 GTGCGTGGCAACAATTGGGATGGTTAATCCATGAATTCGCACATCATCAGTTGTTCAA 582

.....

Db	481	GTTCGCTGGCAACAATTGGGATGGTTAAATCCATGAATTCGCACATCATCAGTTGTTCTCAA	540
Qy	583	AACAGATACTACAAATGATTTGGCCAGCACTATTTCTGGTGGAAACATTTTTTACAAGGATTCCTCA	642
Db	541	AACAGATACTACAAATGATTTGGCCAGCACTATTTCTGGTGGAAACATTTTTTACAAGGATTCCTCA	600
Qy	643	TCCTGGTGGTGGAAAGAGCAGCAACAATGTGCATCAGCAGCCCAAAATGTTGTTGGACGA	702
Db	601	TCCTGGTGGTGGAAAGAGCAGCAACAATGTGCATCAGCAGCCCAAAATGTTGTTGGACGA	660
Qy	703	GACGGAGATCTTCATTTAGTCCCAATCTATGCTACAGTGGCAGACACATCTCAACAATTAT	762
Db	661	GACGGAGATCTTCATTTAGTCCCAATCTATGCTACAGTGGCAGACACATCTCAACAATTAT	720
Qy	763	TCACAGGATTCATGGGTTATGACTCTATTCAGATGGCAACATGTTCAATTCGACATTCATG	822
Db	721	TCACAGGATTCATGGGTTATGACTCTATTCAGATGGCAACATGTTCAATTCGACATTCATG	780
Qy	823	TTACCAATTCCTCGTCTCTCGTGGCTTCCTTCAGTCAATCAATTTTGTAGTCAGATGCCA	882
Db	781	TTACCAATTCCTCGTCTCTCGTGGCTTCCTTCAGTCAATCAATTTTGTAGTCAGATGCCA	840
Qy	883	ACTCATTATTATGACTATTACAGAAATACATGCGATTTATGAACAGGTTGCTCTCTCTTTG	942
Db	841	ACTCATTATTATGACTATTACAGAAATACATGCGATTTATGAACAGGTTGCTCTCTCTTTG	900
Qy	943	CACCTGGGCTGGTCATTTGGGTCAATTTGATTTCTACCCGATTTGGTCAACTAGAAATATG	1002
Db	901	CACCTGGGCTGGTCATTTGGGTCAATTTGATTTCTACCCGATTTGGTCAACTAGAAATATG	960
Qy	1003	TTCTCTCCTCTGTTTCTCATCTCTGTTGGAGGTTTCTGCTCTCTCATGTFAGTTACTTTCAAT	1062
Db	961	TTCTCTCCTCTGTTTCTCATCTCTGTTGGAGGTTTCTGCTCTCTCATGTFAGTTACTTTCAAT	1020
Qy	1063	CATTATTACAGTGAGGAAGTTTGCATTTGAGCTCGAACATCATGTCAAAATTCAGCTTGTCTT	1122
Db	1021	CATTATTACAGTGAGGAAGTTTGCATTTGAGCTCGAACATCATGTCAAAATTCAGCTTGTCTT	1080
Qy	1123	CAAAATCATGACCAACAAGAAATATGAGACCTCGGAAGATTCATTGACCTGGCTTTGGGAGGT	1182
Db	1081	CAAAATCATGACCAACAAGAAATATGAGACCTCGGAAGATTCATTGACCTGGCTTTGGGAGGT	1140
Qy	1183	CTTTAACTATCAGATTTGAGCACCATTCTTTTCCCAACGATGCCAGACACAACCTTGAACACT	1242
Db	1141	CTTTAACTATCAGATTTGAGCACCATTCTTTTCCCAACGATGCCAGACACAACCTTGAACACT	1200
Qy	1243	GTTATGCGACCTTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCGACGAT	1302
Db	1201	GTTATGCGACCTTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCGACGAT	1260
Qy	1303	TATTTTCACAGGATTCGCGCTTGAATTTGACAAATTCGGAATATTTGCAAAATGTTGCTGCT	1362
Db	1261	TATTTTCACAGGATTCGCGCTTGAATTTGACAAATTCGGAATATTTGCAAAATGTTGCTGCT	1320
Qy	1363	AAATTTGACTAAAAAGATTTGCCTAG	1386
Db	1321	AAATTTGACTAAAAAGATTTGCCTAG	1344

### RESULT 3

AAX76589

XX  
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COCO / MARY ST[illegible]XX  
XX  
17 11 1955 (1155 1111)

XX  
KW Caenorhabditis elegans; C. elegans; Delta 6 desaturase; Cebp6.1.;  
KW gamma-linolenic acid; GLA; plant fatty acid; octadecatetraenoic  
KW OPA; eicosanoid; eczema; mastalgia; atherosclerosis; coronary  
KW hypercholesterolaemia; diabetic neuropathy; viral infection; ac  
KW

hypertension; cirrhosis; cancer; ss.

**Caenorhabditis elegans.**

Key	Location/Qualifiers
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CDS 1

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/*tag= a
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WO9927111-A1.

03-JUN-1999.

24-NOV-1998: 98W0-GB03507

24 - NOV - 1997. 97CB-002A783

(UVR-) UNIV BRISTOL.

Number TA:

**FIFTY - 1000-37006 / 21**

WPI: 1999-370905/  
P-PCNB: AAY17751

Desaturase enzymes, the genes encoding them and their uses

Claim 29: Fig 1: 44pp: English.

The present sequence encodes *Caenorhabditis elegans* Delta 6 desaturase, designated Ceb6.1. Desaturase enzymes (I) may be used as immunogens to raise and select antibodies (which may be used in immunossays, and diagnostic tests to detect the presence of (I) in a sample, or to purify (I)) or as a selectable marker for transformation, especially transformations involving plants. (I) can be used to produce gamma-linolenic acid (GLA) (and derivatives of it), which is a high value plant fatty acid that is widely used in medicine for the preparation of compositions for treating disorders associated with deficiencies in GLA or deficiencies in metabolites derived in vivo from GLA, such as octadecatetraenoic acid (OTA) and eicosanoids. Disorders that may be treated with GLA and OTA include eczema, mastalgia, atherosclerosis, hypercholesterolaemia, coronary disease, diabetic neuropathy, viral infections, acne, hypertension, cirrhosis and cancer. The nucleotide sequences (II) encoding (I) may be used as probes or primers. Probes may be used to identify and purify nucleic acids and so may be used in diagnosis to detect the presence of (II) in a sample. Primers are useful for amplifying DNA by polymerase chain reaction (PCR). (II) may also be used to prepare an organism that is either chill resistant or that accumulates GLA or metabolites derived from GLA. Hybridizing DNA molecules may be used as anti-sense molecules to alter the expression of (II) by binding to it and preventing transcription. Hybridizing molecules may also be provided as ribozymes which regulate expression by cleaving RNA molecules.

Sequence 1463 BP; 445 A; 288 C; 277 G; 453 T; 0 other;

very Match 23.8%; Score 348.2; DB 20; Length 1463;

st Local Similarity 55.8%; Pred. No. 3.1e-83;

Matches 712; Conservative 0; Mismatches 553; Indels 12; Gaps 2;

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79 ATTAATAATGATGGAAATGGTGTCAAAATTGACGATGCTGTCTGAGATCACATCCAGT 138

44 ATGAAGGTCGATGGCAAAATGGCTCTACCTTAGCGAGGAATTGGTGAAGAAACATCCAGGA 103

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139 GGTAGTGCATTACTACCTATATAAAATATGGATGCCACTACCGTATTCACACATTCCAT 198

104 CCGCCTTATTGACACATATACAAATTCCCAATCCCATTCCTCCCTTTCC

104 GGAGCGTGTATTGAAACAATATAGAAATTCGGATGCTACTCATATATTTCACGCTTTCCAC 163

199 ACTGGTTCTAAAGAAGCGTATCAATGGCTGACAGAATTGAAAAAGAGTGCCCTACACAA 258

```

RESULT 4
AA51233
ID   AAA51233 standard; cdna; 1275 BP.
XX
AC   AAA51233;
XX
DT   26-SEP-2000 (first entry)
XX
DE   E. gracilis fatty acid delta-8 desaturase coding sequence.
XX
KW   Fatty acid delta-8 desaturase; polyunsaturated; oil; seed;
KW   infant formula; dietary supplement; ss.
XX
OS   Euglena gracilis.
XX
FH   Key
FT   CDS
FT   Location/Qualifiers
FT   14..1273
FT   /*tag= a
FT   /trans_except= (pos:71..75, aa:ValSerAlaIrrp)
FT   /product= Fatty_acid_delta-8_desaturase
XX
PN   WO200034439-A1.
XX
PD   15-JUN-2000.
XX
PF   06-DEC-1999; 99WO-US28655.
XX
PR   07-DEC-1998; 98US-O111301.
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PA   (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI   Browse JA, Wallis JG, Watts JL;
XX
DR   WPI; 2000-431293/37.
XX
P-PSDB; AAY96722.
XX
PT   Purified protein having desaturase activity, useful for creating a
PT   double-bond between two carbons
XX
PS   Claim 8; Fig 7B; 74pp; English.
XX
CC   This cDNA encodes Euglena gracilis fatty acid delta-8 desaturase.
CC   The sequence is useful for recombinant production of the enzyme and for
CC   generating transformed host cells and transgenic plants. The desaturase
CC   can be used for creating a double-bond between two carbons. In
CC   particular, the enzyme is useful for producing polyunsaturated fatty
CC   acids and for generating enzyme-specific antibodies useful for
CC   identifying desaturases. Oil-seed plants may be engineered to incorporate
CC   the enzyme, so that the plants produce seed oil rich in fatty acids. The
CC   fatty acids could be incorporated usefully into infant formula, foods of
CC   all kinds, dietary supplements, nutraceutical and pharmaceutical
CC   formulations.
XX
SQ   Sequence 1275 BP; 294 A; 326 C; 327 G; 328 T; 0 other;

Query Match
Best Local Similarity 7.4%; Score 108.8; DB 21; Length 1275;
Matches 352; Conservative 0; Mismatches 357; Indels 9; Gaps 2;

QY   532 CAACAATTGGGATGTTAATCCATGATTCGACATCATCATGTTTCAAAAACAGATAC 591
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   419 CAACAGATGGGTGGCTTCTCATGATTTGCCACACACACATTTTCAAGAACCGGAC 478
QY   592 TACAATGATTTGGCCAGCTATTTTCGTTGGAATTTTACAAGATTTCTCATCTGGTGT 651
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   479 TGAACAACCTCTGGGACTGGTATTGTCATTTGGTCTGCAAGGTTTTTCCGTGACATGT 538
QY   652 TGAAGAAGACGACCAATGTCATCGACGACGACCAAAATGTTGTTGGACGAGACGGAGAT 711
DB   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   539 TGGNAGGACGACGACCAATGTCATCATTTGGCAACCAATGTTCAAGGGACGACCCGTAT 598
QY   712 CTTGATTTAGTCCCATTTCTATGCTACAGTGGCGAGAACATCTCAACAATTTATCTCAGGAT 771

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Db   599 ATTGACAACTCCCCCTTAGCTGTGAGATGACGTCACACGGGCTCACCGATT 658
QY   772 TCATGGGTTATGACTCTATTTCAGATGGCAACATTTTCATTGGACATTCATGTTACCATTC 831
Db   659 TCCCGCAAGCTCATTCAGTTC-----CAGCAGTACTATTCTTGGTCTATCTGATCTG 712
QY   832 CTCGGTCTCTCGTGGGCTTCTTCAGTCAATCATTTTGTAGTCAGATGCCAACATCATTTAT 891
Db   713 TTGCGGTTTCATTTGGTGTTCAGTGTGCTGTGACCGTGGCGAGTTTGAAGGACAGAGAT 772
QY   892 TATGACTATTACAGAAATACTGCGATTTATGAACAGGTTGCTCTCTCTTTGCACCTGGGCT 951
Db   773 AACCAATTCTATCGCTCTCAGTATAGAAGAGAGGCCATTGGCCTCGCCCTGCACCTGGACC 832
QY   952 T---GGTCAATTGGGTCAATTTATTCCTACCCGATTGGTGAACATAGATAATATGTTCTTC 1008
Db   833 TTGAAGGCCCTGTTCACACTTATTTATGCCCAGCATCTCCATCATCTGCTGTGGTGT 892
QY   1009 CTTGTTCTCATCTGTTGGAGTTTCTGCTCTCTCTCATGATGATGATTTTCAANTCATTTAT 1068
Db   893 TTCGTTTCGGAGCTGTTGGCGCTTCGGCATTCGCGATTCGTTGTTTTCGAGGCTTGAAT 1072
QY   1069 TCAGTGGAGAAAGTTTGCAATTGAGCTCGAACATCATGTCAAATTTACGCTTGTCTTCAAATC 1128
Db   953 CCACTGGAGAAGATCGGGACCCAGTCTGGGATGCCATGGATTCGCTGGTGGCCAGATC 1012
QY   1129 ATGACCACAAGAATATGAGACCTGGGAAGATTTCATTGACTGGCTTTGGGGAGGCTTTAAC 1188
Db   1013 CATGAGACCATGAACATTCGCGAGGATTTATCAGATTTGTTTTCGGAGGCTTGAAT 1072
QY   1189 TATCAGATTGAGCACCATTCTTTCCCAACGATGCCAGCAGACACACTTGAACACTGTTA 1246
Db   1073 TACCAGATTGAGCACCATTGTTGGCCGACCCCTCCCTCGCCACAACCTGACACGCGTTA 1130

RESULT 5
AAF25734
ID   AAF25734 standard; DNA; 2160 BP.
XX
AC   AAF25734;
XX
DT   06-APR-2001 (first entry)
XX
DE   C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 11.
XX
KW   Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW   transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW   cosmetic; ds.
XX
OS   Ceratodon purpureus.
XX
FH   Key
FT   CDS
FT   Location/Qualifiers
FT   159..1721
FT   /*tag= a
FT   /product= "delta6-acetylenase/delta6-desaturase"
XX
XX
WO2000075341-A1.
XX
PD   14-DEC-2000.
XX
PF   07-JUN-2000; 2000WO-EP05274.
XX
PR   07-JUN-1999; 99DE-1025718.
PR   22-DEC-1999; 99DE-1062409.
XX
PA   (BADI ) BASF AG.
XX
PI   Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;
XX
DR   WPI; 2001-112150/12.
DR   P-PSDB; AAB46440.
XX

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**Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids**

Claim 1a; Page 54-57; 69pp; German; German.

This invention describes a novel isolated nucleic acid (I), encoding polypeptides (II) with delta6-acetylase and/or delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids.

Sequence 2160 BP; 509 A; 481 C; 556 G; 614 T; 0 other;

[illegible]

Db	1445	CTTCGTG-----AATGCCAGATTGCATCGACTCCGACATCAACGACGGGT	1492
Qy	1158	ATTCAATTGACTGGCTTTGGGAGGTCTTAATACTATCAGATTGAGCACCATCTTTTCCCAAC	1217
Db	1493	GTTTAATGATTGGTTCCACCGAGGTCTCAACAGACAGATTGAGCATCATCTATTTCACAC	1552
Qy	1218	GATGCCACGACACAACACTTGAACACTGTTATGCCCACTGTGTTAAGGAGTT	1265
Db	1553	GATGCCCGACGACAAACCTTAATAAAATTTCTCCTCAGTGGAGACTTT	1600
RESULT 6			
AAF26040			
XX	AAF26040 standard; cdna; 2012 BP.		
XX	AAF26040;		
XX	23-APR-2001 (first entry)		
DT	P. patens delta6-desaturase cdna.		
DE			
DE			
XX			
KW	Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;		
KW	fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;		
KW	agricultural chemical; ds.		
XX			
OS	Physcomitrella patens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	319..1896	
FT		/*tag= a	
FT		/product= "delta6-desaturase"	
XX			
PN	WO200102591-A1.		
XX			
PD	11-JAN-2001.		
XX			
PF	04-JUL-2000; 2000WO-EP06223.		
XX			
PR	06-JUL-1999; 99US-0347531.		
PR	30-JUN-2000; 2000DE-1030976.		
XX			
PA	(BADI ) BASF AG.		
XX			
PI	Heinz E, Girke T, Scheffler J, Da Costa Silva EO;		
XX			
DR	WPI: 2001-123117/13.		
DR	P-PSDB: AAB46810.		
XX			
PT	Production of unsaturated fatty acids, useful e.g. in nutrition,		
PT	cosmetics or pharmaceuticals, in organisms transformed with		
PT	Physcomitrella patens delta-6-desaturase nucleic acid -		
XX			
PS	Claim 1a; Page 38-41; 49pp; German.		
XX			
CC	This invention describes a novel preparation of unsaturated fatty acids		
CC	(I) by introducing into an organism at least one isolated nucleic acid		
CC	(II) that encodes a polypeptide (III) with Delta6-desaturase activity.		
CC	Organisms that contain at least 1 wt. % (I), on total fatty acid content,		
CC	are then selected. (II) is selected from: (a) a 2012 bp sequence (S1),		
CC	defined in the specification, or its equivalents within the degeneracy of		
CC	the genetic code; or (b) derivatives of the sequence of (a) that encode a		
CC	525 amino acid polypeptide (S2), defined in the specification, or a		
CC	polypeptide with at least 50% homology with (S2) and practically the same		
CC	enzymatic activity. The invention also describes (1) transgenic organisms		
CC	that contain (II); and (2) oils, lipids and fatty acids produced by the		
CC	new method. The oils, lipids and fatty acids produced by the transformed		
CC	organisms are used in human or animal nutrition, cosmetics,		
CC	pharmaceuticals and agricultural chemicals. (III) can also be used, in		
CC	vitro, for increasing the (I) content of triglycerides. The transgenic		
CC	organisms have increased contents of (I), or of (I)-containing		
CC	triglycerides, particularly of gamma-linolenic acid.		
XX			
Sequence	2012 BP; 482 A; 427 C; 553 G; 550 T; 0 other;		
XX			

Query Match 5.68; Score 82.4; DB 22; Length 1012;  
 Best Local Similarity 46.18; Pred. No. 8.2e-12;  
 Matches 398; Conservative 0; Mismatches 451; Indels 15; Gaps 3;

QY 498 TCTTCATCAGCTATTCTAATGGGAGTGGTGGCAACAATGGGATGGTTAATCCATGA 557  
 DB 1023 TTTGGCTTACGCTGATGATGCTGCTGTTTCCACACATGGGATGGTATCCCATGA 1082

QY 558 ATTCGCACATCATCAGTTGTTCAAAACAGATACATCAATGATTTGGCCAGCTATTCGT 617  
 DB 1083 TTTTCTCCCAATCAGGTGTTTGAGACACGCTGGCTTAATGAAGTTCGCGGTATGAT 1142

QY 618 TGAAGAATTTTACAGGATCTCATCTGCTGGTGGAAAGACAGCAGACATGCGATCA 677  
 DB 1143 CGCAGACGCGTCTGGGGTTTATGACAGGGTGGTGAAGGAAGCATACCTTCATCA 1202

QY 678 CGCAGCACAAATGTTGTTGGAGGAGACGAGATCTTGATTTAGTCCCATTCATGCTAC 737  
 DB 1203 TGCTGCTCCAAATGAATCGCATCAGATTACCAACCAATGATGAAGATATTGATCTCT 1262

QY 738 AGTGGCAGAACATCTCAACAATATTCTCAGGATTCATGGGTTATGACTCTATTCAGATG 797  
 DB 1263 CCCTCTCAATGCTGGAGCAAGGACATCTGCGCACAGTTGAGAATAAGACATTC--TTG 1320

QY 798 GCAACATGTTTCATGACATTCATGTTACCATCTCCGCTCTCGTGGCTTCTTCAGTC 857  
 DB 1321 CGAATCCTCAATACCAGCATCTGTTCTTCATGGGCTGTTATTTTCGCGCTGGTAGT 1380

QY 858 AATCATTTTGTAGTCAGATGCAACTATTATTATGACTATTACAGAAATCTCGAT 917  
 DB 1381 TGCTCTTTTGGAGCTGGAGATATCTCTACAGAGTGTCTCACCTGTCGACAG-GTT 1439

QY 918 TTATGAACAGTTGGTCTCTCTTTGTCACATGCTTGGTCAATGGGTCATTTGATTTCC 977  
 DB 1440 GTTGAAGAAGGAATCTGTTCTCACTACTTTTGGTTCGTCGGGACACGCTATCT 1499

QY 978 ACCGATTTGGTCACTAGATATGTTCTCTCTGTTTCTCNCATCTGTTGGAGGTTCC 1037  
 DB 1500 TCTCCCTGTTGGAAGCCATTTAGTATGGATGGCGGTGACTGACCTCATGTCGGCATGCT 1559

QY 1038 GCTCTCTCATGTAGTTTACATTTCAATCATATTTCAGTGGAGAAAGTTTGCAFTGAGTCGAA 1097  
 DB 1560 GCTGGCTTTGTATTGTTACTTAGCCACAATGGATGGAGTTTAT-----AA 1607

QY 1098 CATCATGTCAAATACGTTGCTTCAATCATATGACCAACAAAGAAATATGAGACCTGGAAG 1157  
 DB 1608 TTGCTCTAAAGAAATTCGTAGTGCACAGATCGTATCCACACGGGATATCAAGAAACAT 1667

QY 1158 ATTCATTTGACTGGCTTTGGGAGGCTTAACTATCATAGATTGACACCATCTTTTCCCAAC 1217  
 DB 1668 ATTCACAGCTGCTTCACTGGTGGCCCTTAACAGGCAATAGAGCATCATCTTTCCCAAC 1727

QY 1218 GATGCCACGACAACTTGAACACTGTTATGCCCACCTGTTAAGGAGTTTGCACAGCAAA 1277  
 DB 1728 AATGCCAGGCATTAATTTAAACAATAAGCACCTAGAGTGAGGTTCTGTGAAGAAACA 1787

QY 1278 TGGTTTACCATACATGGTGCAGCATTTATTTACAGGATTTCTGGCTTGAATTTGAGCAAT 1337  
 DB 1788 CGGTCTGGTGTAGGAAGACGATCTATTGCTACCGGCACCTTGCAGGTTTGAAGCAT 1847

QY 1338 CCGAATATTGCAATGTTGCTGC 1361  
 DB 1848 GAAGGAAGTCGGGAGGCTCGGC 1871

RESULT 7  
 AA247129  
 ID AA247129 standard; DNA; 1374 BP.  
 XX  
 AC  
 AA247129;  
 XX  
 28-MAR-2000 (first entry)

XX Fungal delta6-desaturase coding sequence.  
 DE Polynunsaturated fatty acid; fungus; delta6-desaturase; animal feed;  
 XX transgenic animal; malnutrition; biosynthesis; ds.  
 KW Unidentified.  
 OS WO9961602-A1.  
 PN 02-DEC-1999.  
 XX 28-MAY-1999; 99WO-US12088.  
 XX 29-MAY-1998; 98US-0087578.  
 PR (OHIS ) UNIV OHIO STATE.  
 XX Kopchick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;  
 DR WPI; 2000-072619/06.  
 XX P-PSDB; AAY56045.  
 PT Producing essential fatty acids and long-chain polyunsaturated fatty  
 PT acids, for use in nutritional, animal feed and medical formulations -  
 XX Disclosure; Fig 8; 71pp; English.  
 XX The invention relates to a method of generating novel compositions  
 CC comprising animal cells producing essential fatty acids (FAs). The animal  
 CC cells are produced by transforming cells, e.g. embryonic stem cells, with  
 CC nucleic acid encoding heterologous enzymes involved in fatty acid, this  
 CC e.g. long chain or polynunsaturated fatty acid (PFA) biosynthesis. This  
 CC sequence is an example of such a nucleic acid sequence and encodes a  
 CC fungal delta6-desaturase. The essential FAs obtained can be used in  
 CC nutritional formulations or animal feed formulations. The long chain PFAs  
 CC can be used in nutritional formulations, cosmetic formulations or animal  
 CC feed formulations. The products can also be used for producing transgenic  
 CC animals which can be used for producing essential FAs which can be used  
 CC for producing downstream products such as leukotrienes, thromboxanes,  
 CC arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid. The  
 CC products can also be used in cell culture. The animal or milk fat  
 CC produced can be administered to treat malnutrition.

QY 500 TTCATCAGCTATTCTAATGGGAGTTCGCTGGCAACAATTTGGGATGGTTAATCCATGAAT 559  
 DB 461 TGCTCTCGGCTGGCTTTTGGTCTGTTCTGGCAGCAGTCGGATGGTTGCTCAGCAT 520

QY 560 TCCGACATCATCAGTTGTTCAAAACAGATACATCAATGATTTGGCAGCTATTTGCTGT 619  
 DB 521 TTTTGGATCACCAGGCTCTCCAGGACCGTTTCTGGGTGATCTTTTGGCGCTCTTTGG 580

QY 620 GAAACATTTTACAGGATTCATCTGCTGGTGGAAAGAGCAGACACAATGTCATCAG 679  
 DB 581 GAGGTGTCGCCAGGCTTCTGCTCTGTTGGTGGAAAGAGCAGACACAATCACCACG 640

QY 680 CAGCCACAATGTTGTTGGAGCAGACGAGATCTTGATTTAGTCCCATCTATGCTACAG 739  
 DB 641 CCGCCCCCAACGTCACGCGGAGGATCCCGACATTGA--CACCACCTCTGTTGACCTG 698

QY 740 TGGCAGAAATCTCAACAATTTCTCAGGATTCATGGGTTATGACTCTATTCAGATGGC 799  
 DB 699 GAGTGAGCATGCTTGGAGATGTTCTCGGATGTCAGATGAGGAGCTGACCCGCTATG 758

QY 800 AACATGTTTATGGACATTT-----CATGTTACCATTTCTCTCCG 836  
 DB 759 GTCGCGTTTTCATGCTCCTGAACACAGACCTGTTTACTTCCCATCTCTCTGTTGCGCG 818

Query Match 5.18; Score 73.8; DB 21; Length 1374;  
 Best Local Similarity 47.58; Pred. No. 1.4e-09;  
 Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;

QY 837 TCTCTGCGGCTCTTTCAGTCAATCATTTTGTAGTCAGATGCCAACTCATTTATGA 896  
 DB 819 TCTCTCTGGTCCCTCCAGTCCATCTCTTTGTGCTGCTAACGGTCAGGCCCAAGCC 878  
 QY 897 CTATTACAGAAAT-----ACTGGGATTTATCAACAGGTTGGTCTCTTTTGGCACTGGCC 950  
 DB 879 CTCGGGCGCGGTGTGCCCATCTCGTTGGTCGAGCAGCTGTCGCTTGGATGCTGAC 938  
 QY 951 TTGGTCATGGGTCAATTTGT---ATTTCCTACCGGATGGTCAACTGAATAAAGTTCTT 1007  
 DB 939 CTGGTACCTGCCCACTGTTCTCTGTTTCATCAAGGATCCCGTCAACATGCTGGTACTT 998  
 QY 1008 CTTGTTTCTCATCTTGTGGAGTTTCTCTCTCTCATGTAGTACTTTCAATCAATTA 1067  
 DB 999 TTTGGTGTCCGAGCGGTGTGGGAACTTTGTGGGATGCTGTCTCGCTCAACCAAA 1058  
 QY 1068 TTCAGTGAGAAAGTTTGCATTCAGCTCGAAGCATCATGTCAAAATACGCTTGTCTTCAAT 1127  
 DB 1059 CGGTATGCTCTGATCTCGAAGGAGGCGGTGATATGATTTCTTTCACGAAGCAGAT 1118  
 QY 1128 CATGACCACAGAAATATGACACCTGGAAGATTTCATTCAGTCTGGCTTTGGGAGGCTTAA 1187  
 DB 1119 CATCAGGGTCTGATGTCCACCGGGTCTATTTGCCAACTGGTTTCACGGGTGGATTGAA 1178  
 QY 1188 CTATCAGATTGAGCACCATTCTTTCCCAACGATGCCAGACACAACTTTGAACACTGTTAT 1247  
 DB 1179 CTATCAGATCAGCACCATTGTTCCCTTCGATGCTCGCTGCCCAACTTTTCAAGATCCA 1238  
 QY 1248 GCCACTTGTAAAG 1260  
 DB 1239 GCCTGCTGTCGAG 1251

## RESULT 8

AAF25234  
 ID AAF25234 standard; DNA; 1374 BP.  
 AC AAF25234;  
 XX 30-APR-2001 (first entry)  
 DT Nucleotide sequence of a fungal delta6 desaturase.  
 XX  
 DE delta6 desaturase; desaturase gene; elongase gene; fatty acid;  
 KW eicosanoid; nutrition; infant formula; dietary supplement;  
 KW dietary substitute; animal feed; ss.  
 XX  
 OS Mortierella alpina.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1374  
 FT /\*tag= a  
 FT /product=. "delta6 desaturase"  
 XX  
 PN WO200104636-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 11-JUL-2000; 2000WO-US19011.  
 XX  
 PR 12-JUL-1999; 99US-0351525.  
 XX  
 PA (UOVH-) UNIV OHIO.  
 XX  
 PI Kopchick JJ, Kelder B;  
 XX  
 DR WPI; 2001-182622/18.  
 DR P-PSDB; AAB31684.  
 XX  
 PT New compositions comprising cells that express desaturases and  
 PT elongases, for synthesizing essential fatty acids or long-chain  
 PT polyunsaturated fatty acids, used in nutritional, cosmetic or animal

## PT feed formulations -

XX Disclosure: Fig 8; 93pp; English.

XX The present sequence encodes a delta6 desaturase. The desaturase  
 CC polynucleotide sequence was used to transfect mammalian cells, to  
 CC produce animal cells expressing a desaturase gene and/or an elongase  
 CC gene. Compositions comprising cells of the invention are useful for  
 CC synthesizing essential fatty acids, their derivatives or downstream  
 CC products, as well as altered levels of long-chain polyunsaturated  
 CC fatty acids and eicosanoids. The compositions are useful in nutritional  
 CC formulae, e.g. infant formula, dietary supplements or dietary  
 CC substitutes for both humans and animals. The compositions are also  
 CC useful in cosmetic or animal feed formulations. Furthermore, the  
 CC compositions may also be used as fat free media or as research reagents.

XX Sequence 1374 BP; 257 A; 386 C; 378 G; 353 T; 0 other;

## Query Match

Best Local Similarity 5.1%; Score 73.8; DB 22; Length 1374;

Mismatches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;

QY 500 TTCATCAGCATATTAATGGAGTTGGTGGCAACAATTTGGATGGTTAATCCATGAAT 559  
 DB 461 TGTCTCGCTCGCGCTTTTGGTCTGTCTTGGCAGCAGTGGTGGCTCAGACT 520  
 QY 560 TCGCATCATCAGTTGTTCAAAAACAGATACATGATTTGGCCAGCTATTTCTGTTG 619  
 DB 521 TTTTCATCACCAGGTCTTCCAGGACGTTCTGGGGTGATCTTTTGGCGGCTTTGG 580  
 QY 620 GAAACTTTTACAGGATTTCTCATCTGGTGGTGGAAAGAGCAGCAATGTGCATCAG 679  
 DB 581 GAGGTGCTGCCAGGCTTCTGCTCTGCTGGTGGAGGACAGACACACTCACCACG 640  
 QY 680 CAGCCACAATGTTTGGACGAGAGGAGATCTTGATTTAGTCCCATCTCTATGCTACAG 739  
 DB 641 CCGCCCCCAACGTCACGCGAGGATCCGACATTTGA--CACCCACCTCTGTTGACCTG 698  
 QY 740 TGGCAGAACATCTCAACAATTTCTCAGGATTCATGGGTATGACTCTATTCAGATGC 799  
 DB 699 GAGTGAGCATGCGTTGGAGATCTTCTCGGATGTCAGATGAGGAGCTGACCGCATGTG 758  
 QY 800 AACATGTTCAATGGACATTT-----CATGTTACCATTTCTCTCCG 836  
 DB 759 GTCGGTTCATGGTCTTGAACACGACCTGGTTTACTTCCCATCTCTCGTTGCCCG 818  
 QY 837 TCTCTCGTGGCTTCTTCAGTCAATCATTTTGTAGTCAGATGCCAACTCATTTATGA 896  
 DB 819 TCTCTCTGGTGCCTCCAGTCCATCTCTTTGTGCTGCCCTAACGGTCCAGGCCAAGCC 878  
 QY 897 CTATTACAGAAAT-----ACTGCGATTTATCAACAGGTTGGTCTCTCTTGCACATGGCC 950  
 DB 879 CTCGGGCGCGGTGTGCCCATCTCTGTTGGTCGAGCAGCTGTCGTTGCCATGCACTGGAC 938  
 QY 951 TTGGTCAATGGGTCAATTTGT---ATTTCCTACCGGATTTGGTCAACTAGATAATGTTCTT 1007  
 DB 939 CTGGTACCTGCCCACTGTTCTCTGTTTCATCAAGGATCCCGTCAACATGCTGGTACTT 998  
 QY 1008 CTTGTTTCTCATCTTGTGGAGGTTTCTGCTCTCTCATGTAGTACTTTCATCATTA 1067  
 DB 999 TTTGGTGTCCGAGCGGTGTGCCGAACTTTGTTGGGATGCTGTCTCGCTCAACCAAA 1058  
 QY 1068 TTCAGTGAGAAAGTTTGGATTTGAGCTCGAAGCATCATGTCAAAATACGCTTCTTCAAT 1127  
 DB 1059 CGGTATGCTGTGATCTCGAAGGAGGCGGTGATATGATTTCTTTCAGGAAGCAGAT 1118  
 QY 1128 CATGACCACAGAAATATGAGACCTGGAAGATTCATTTGACTTGTGGGAGGCTTAA 1187  
 DB 1119 CATCAGGGTCTGATGTGCCACCGGGTCTATTTGCCAACTGGTTCCAGGGGTGATGA 1178  
 QY 1188 CTATCAGATTGAGCACCATTCTTTCCCAACGATGCCAGACACAACTTTGAACACTGTTAT 1247  
 DB 1179 CTATCAGATCAGCACCATTGTTCCCTTCGATGCTCGCTGCCCAACTTTTCAAGATCCA 1238

QY 1248 GCCACTGTTAAG 1260  
 DB 1239 GCCTGCTGCGAG 1251

RESULT 9  
 AAV63624

ID AAV63624 standard; cDNA; 1617 BP.  
 AC AAV63624;  
 XX  
 DT 15-FEB-1999 (first entry)  
 DE cDNA encoding a delta-6 desaturase enzyme.  
 XX

KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;  
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 KW cholesterol level; endometriosis; premenstrual syndrome;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.  
 XX

OS Mortierella alpina.  
 XX

FH Key Location/Qualifiers  
 FT 71..1444  
 FT /\*tag= a  
 FT /product= delta-6 desaturase  
 XX

PN W09846763-A1.  
 XX

PD 22-OCT-1998.  
 XX

PF 10-APR-1998; 98WO-US07126.  
 XX

PR 11-APR-1997; 97US-0834655.  
 XX

PA (ABBO ) ABBOTT LAB.  
 PA (CALJ ) CALGENE LLC.  
 XX

PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;  
 PI Thurmond J;  
 XX

DR WPI; 1998-594582/50.  
 DR P-PSDB; AAW84137.  
 XX

PT New isolated fatty acid desaturase enzymes - used for the production  
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical  
 PT compositions, nutritional compositions, cosmetics or animal feed  
 XX

PS Claim 1; Fig 3A-E; 165pp; English.  
 XX

CC The present sequence encodes a Mortierella alpina fatty acid delta-6  
 CC desaturase enzyme. The enzyme sequence is used in the methods of  
 CC the invention. The specification describes methods for desaturating a  
 CC fatty acid and for producing a desaturated fatty acid by expressing  
 CC increased levels of a desaturase. The present desaturase is an enzyme  
 CC which introduces a double bond carbons 6 and 7 from the carboxyl end of  
 CC a fatty acid molecule. The enzyme can be used for desaturating fatty  
 CC acids. The enzyme can be used to produce polyunsaturated fatty acids,  
 CC which can be used for treating malnutrition, in pharmaceutical  
 CC compositions, in cosmetics or in animal feed. The polyunsaturated fatty  
 CC acids can be used for treating e.g. restenosis after angioplasty,  
 CC inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes  
 CC or eczema or reduce blood pressure. They can also be used to inhibit  
 CC platelet aggregation, cause vasodilation, lower cholesterol levels,  
 CC inhibit proliferation of vessel wall smooth muscle and fibrous tissue,  
 CC reduce or prevent gastro-intestinal bleeding and other side effects  
 CC caused by non-steroidal anti-inflammatory drugs, prevent or treat  
 CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis  
 CC and chronic fatigue after viral infections, treat AIDS, multiple  
 CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin

CC disorders.  
 XX  
 SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;  
 Query Match 5.1%; Score 73.8; DB 19; Length 1617;  
 Best Local Similarity 47.5%; Pred. No. 1.5e-09;  
 Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;  
 QY 500 TTCCATCAGCTATTCTAATGGGAGTTGCGTGGCAACAATTTGGGATGTTTAAATCAATGAAT 559  
 DB TGTCTCGGCTCGGCTTTTGGGCTCTCTCTGCGAGCAGTCGCGGATTTGGCTCAGCACT 590  
 QY 560 TCGCACATCATCAGTTGTTTCAAAAACAGATACATACATGATTTTGGCCAGCATTTTCGTTG 619  
 DB TTTTGCATCACCAGGCTCTTCCAGGACCGTTTCTCGGGTGATCTTTTCGGGCGCTCTCTTGG 650  
 QY 620 GAAACTTTTACAGGATTTCTCATCTGGTGGTGGAAAGACGACACAATGTGCATCAGC 679  
 DB 651 GAGGTCTCTGCCAGGCT 710  
 QY 680 CAGCCACAATGTTGTTGGACGAGAGATCTTGATTTAGTCCCATTTCTATGCTACAG 739  
 DB 711 CCGCCCCCAACGTCACGCGGAGGATCCCGACATTGA--CACCCACCTCTGTTGACCTG 768  
 QY 740 TGGCAGAACATCTCAACAATTTATCTCAGGATTCATGGGTTATGACTCTATTCAGATGGC 799  
 DB 769 GAGTGAGCATGCGTTTGGAGATGTTCTCGGATGTTCCAGATGAGGAGCTGACCCGATGTG 828  
 QY 800 AACATGTTTCAATGGACATT-----CATGTTACCATTCCTCCG 836  
 DB 829 GTCGGGTTTCATGGTCTCTGAACGACAGCTGGTCTTCTCTCTCTCTCTCTCTCTCTCTCT 888  
 QY 837 TCTCTCGTGGCTTCTTCAGTCAATCATTTTGTAGTCAGATGCCAACTCATTTATATGA 896  
 DB 889 TCTCTCTGCTGCTCCAGTCCATCTCTTTGCTGCTGCTAACGGTCAGCGCCACACAGCC 948  
 QY 897 CTATTACAGAAAT-----ACTGCGATTTATGAACAGGTTGCTCTCTCTCTCTCTCTCTCT 950  
 DB 949 CTCGGCGCGCGTGTGCCCATCTCTGTTGGTCGAGCAGCTGCTGCTTCCGATGCACTGGAC 1008  
 QY 951 TTGGTCAATTTGGGTCATTTGT---ATTCTCTACCCGATTTGGTCAACTAGATAATATGTTCTT 1007  
 DB 1009 CTGTTACTCTGCCACCATCTTCTCTCTATCAAGGATCCCGTCAACATGCTGGTGTACTT 1068  
 QY 1008 CCTTGTCTCTATCTTTGAGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1067  
 DB 1069 TTTGGTGTGCGAGCGGTGTGCGGAAACTTTGTTGGCGATGCTGTCTCTCGCTCAACCACAA 1128  
 QY 1068 TTCAGTGGAGAAGTTTGCATTTAGCTCGAACATCATGTCMAATTTACGCTTGTCTTCAAT 1127  
 DB 1129 CGGTATGCTGTGATCTCGAAGGAGGCGGTCGATATGATTTCTTTCACGAGCAGAT 1188  
 QY 1128 CATGACCACAAGAAATATGAGACCTGGAAGATTCATTGACTGGCTTTGGGAGGTCTTTAA 1187  
 DB 1189 CATTCAGGTCGTGATGTCACCCGGGTCTATTTCGCAACTGGTTCACGGGTGGATTGAA 1248  
 QY 1188 CTATCAGATTGAGCACCACCTTTTCCCAACGATGCCACGACACACAATTTGAACACTGTTAT 1247  
 DB 1249 CTATCAGATCGAGCACCACCTTGTCTCCCTTCGATGCTCGCCACACACTTTTCAAGATCCA 1308  
 QY 1248 GCCACTGTTAAG 1260  
 DB 1309 GCCTGCTGCGAG 1321

RESULT 10  
 AAX00889  
 ID AAX00889 standard; DNA; 1617 BP.  
 XX  
 AC AAX00889;  
 XX  
 DT 26-MAR-1999 (first entry)  
 XX

DE Mortierella alpina delta 6 desaturase encoding DNA.

KW Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;

KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;

KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;

KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;

KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;

KW diabetes; cosmetic; animal feed; ss.

XX Mortierella alpina.

XX

XX Key Location/Qualifiers

FT 71..1443

FT /\*tag= a

FT /product= "delta 6 desaturase"

XX

PN W09846764-A1.

XX

XX 22-OCT-1998.

XX

XX 10-APR-1998; 98WO-US07421.

XX

XX 24-OCT-1997; 97US-0956985.

PR 11-APR-1997; 97US-0833610.

PR 11-APR-1997; 97US-0834033.

PR 11-APR-1997; 97US-0834655.

XX

XX (ABBO ) ABBOTT LAB.

PA (CALJ ) CALGENE LLC.

XX

XX Chaudhary S, Huang Y, Knutzen D, Leonard AE, Mukerji P;

PI Thurmond J;

XX

XX WPI; 1999-080739/07.

DR P-PSDB; AAW95504.

XX

XX Nucleic acid construct able to express fatty acid desaturase in

PT plants - useful in human or animal nutrition, as cosmetics and

PT therapeutically, e.g. for restenosis, cancer and diabetes

XX

PS Claim 1; Fig 3A-E; 210pp; English.

XX

XX This DNA encodes a Mortierella alpina delta 6 desaturase. The invention

CC relates to a nucleic acid construct that contains at least one of the

CC nucleotide sequences (AA00889 to AA00891) encoding M. alpina delta 6,

CC delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively,

CC coupled to an expression control sequence functional in plants.

CC Recombinant plant cells containing at least one DNA encoding a M. alpina

CC fatty acid desaturase (FAD), can be used for the production of

CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants

CC containing them are used to produce oils such as linoleic acid,

CC arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid,

CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are

CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or

CC dietary supplements or substitutes, for use in humans or animals; (iii)

CC for treating disorders associated with inadequate consumption or

CC production of PUFA (or their metabolites such as prostaglandins), e.g.

CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,

CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and

CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate

CC related coding sequences. Recombinant plants can produce high yields of

CC PUFA, since new pathways can be created and unwanted ones suppressed.

CC Plants can be engineered to express oils of particular PUFA composition,

CC e.g. one similar to that in human milk, and product recovery is simpler

CC than with e.g. fish.

XX

XX Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;

SQ

Query Match.

Best Local Similarity 5.1%; Score 73.8; DB 20; Length 1617;

Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;

QY 500 TTCCATCAGCTATTCTATGGAGTGGTGGCGACAAATTGGGATGTTATCCATGAAT 559

Db 531 TGCTCTGGCTGGCTTTTGGTCTGTCTTGGCAGCTGCGATGGTGGCTCAGCACT 590

Qy 560 TCGCACATCATCAGTTGTTTAAAACAGATCTACTACAATGATTTGGCCAGCTATTTCCTGTTG 619

Db 591 TTTTGATCATCAGGAGTCTTCCAGGACCTTCTTGGGTGATCTTTTGGCGCTCTTTGG 650

Qy 620 GAAACTTTTACAAGGATCTCATCTGCTGTTGGAAGAGCAGCAGCAATGTGCATCAGC 679

Db 651 GAGGTGCTGCCAGGCTTCTCGTCTCGTGGTGAAGAGCAAGCACACATCTCACCG 710

Qy 680 CAGCCACAATGTTGTTGGAGGAGGAGATCTTGAATTTAGTCCCATCTTCTATGCTACAG 739

Db 711 CCGCCCCCAAGCTCCAGCGGAGGATCCGACATTGA--CACCCACCTCTGTTGACCTG 768

Qy 740 TGGCAGAAACATCTCAACAATTTATCTCAGGATTTACGGGTTATGACTCTATTTCAGATGCC 799

Db 769 GAGTGAGCATCGGTTGGAGATGTTCTCGGATGTCGCCAGATGAGGAGTGAACCCGATGTG 828

Qy 800 AACATGTTCAATTGGACATT-----CATGTTACCAATCTCTCCG 836

Db 829 GTCCGGTTTCATGGTCTGGAACAGACCTGGTTTACTTCCCATCTCTCGTTGGCCG 888

Qy 837 TCTCTCGTGGCTTCTCAGTCAATCAATTTTGTAGTCAGATGCCAATCTATATATGA 896

Db 889 TCTCTCGTGGTGGCTCCAGTCCATCTCTTGTGCTGCTAACGGTTCAGGCCACCAAGCC 948

Qy 897 CTATTACAGAAAT-----ACTGGGATTTGAACAGGTTGGTCTCTCTTTCGACTGGGC 950

Db 949 CTCGGGCGCGGTGTGCCCATCTCGTTGGTCGAGCAGCTGTCGTTGCGATGCACTGGAC 1008

Qy 951 TTGGTCATTTGGTCAATTTGT--ATTTCCTACCCGATTTGGTCACTAGAAATATGTTCTT 1007

Db 1009 CTGGTACCTCGCCACCATGTTCTCTGTTTCAAGGATCCCGTCAACATGCTGCTGTTACTT 1068

Qy 1008 CTTGTTTCTCATCTTGTGGAGGTTTCTGCTCTCTCATGTTAGTTACTTTTCAATCATTA 1067

Db 1069 TTTGGTGTGCGAGGGGTGTGCGAAACTTGTGGCGATCGTGTCTCTCGCTCAACCACAA 1128

Qy 1068 TTCAGTGGAGAAAGTTTGCATTTGAGCTCGAATCATGTCAAATTTAGCTGTCTTCAAT 1127

Db 1129 CGGTATGCTGTGATCTCGAAGGAGGAGGCGGTGATATGGATTCTTTCACGAAGCAGAT 1188

Qy 1128 CATGCCACAGAATATGAGACCTGGAAGATTCATTGACTGCTGCTTTGGGAGGCTCTTAA 1187

Db 1189 CATCAGCGGTGCTGATGTCCACCCGGGTCTATTTGCCAACTGTTTCAACGGTGGATTGA 1248

Qy 1188 CTATCAGATTGAGCACCACATCTTTTCCCAACGATGCCAGACACAACTTTGAACACTGTTAT 1247

Db 1249 CTATCAGATCGAGCACCACATTTGTTCCCTTCGATGCTCGCCACAACTTTTCAAGATCCA 1308

Qy 1248 GCCACTTGTAAAG 1260

Db 1309 GCCTGCTCTCGAG 1321

RESULT 11

AAA09430

ID AAA09430 standard; DNA; 1617 BP.

XX

AC AAA09430;

XX

XX 10-AUG-2000 (first entry)

DT

XX

DE M. alpina delta-6 fatty acid desaturase coding sequence.

XX

XX delta-6 desaturase; gamma-linolenic acid; biosynthesis;

KW transgenic insect cell; polyunsaturated long chain fatty acid;

KW antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;

KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;

KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;

XX antiaggregant; vasotropic; ss.

XX

OS Mortierella alpina.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 71..1443  
 FT /\*tag= a  
 FT /product= delta-6\_desaturase  
 XX  
 PN WO200020602-A2.  
 XX  
 XX 13-APR-2000.  
 XX  
 XX 29-SEP-1999; 99WO-US22686.  
 XX  
 XX 05-OCT-1998; 98US-0103110.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA  
 XX Mukerji P, Huang Y, Parker-barnes JM, Das T;  
 PI WPI; 2000-328935/28.  
 XX P-PSDB; AAY92599.  
 DR  
 XX  
 XX Novel transgenic insect cells comprising a nucleotide sequences which  
 PT encode delta-6-desaturase or delta-12-desaturase, useful for producing  
 PT polyunsaturated long chain fatty acids, e.g. arachidonic acid  
 XX  
 XX Example 2; Page 144-145; 170pp; English.  
 PS  
 CC The fatty acid desaturases are able to catalyse the conversion of oleic  
 CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of  
 CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells  
 CC comprising a nucleotide sequence which encodes a polypeptide comprising  
 CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6  
 CC desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are  
 CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated  
 CC from the recombinant insect cells are also claimed. Production of  
 CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many  
 CC advantages, as insect cells have greatly simplified lipid compositions,  
 CC are not subject to external variable fluctuations, and can easily be  
 CC maintained and manipulated. The oils are used in pharmaceutical  
 CC compositions, infant formulas, dietary supplements or substitutes, and  
 CC cosmetics (all claimed). The PUFA supplements have antiinflammatory,  
 CC antirheumatic, antischismatic, antipsoriatic, osteopathic, cytostatic,  
 CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,  
 CC hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic  
 CC activity.  
 XX  
 SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;

Query Match 5.1%; Score 73.8; DB 21; Length 1617;  
 Best Local Similarity 47.5%; Pred. No. 1.5e-09;  
 Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;  
 QY 500 TTCATACGCTATTCTAATGGAGTTCGCTGGCAACAATGGGATGTTAATCCATGAAT 559  
 DB 531 TGCTCTCGCTCGCTTTTGGTCTGTTCTGGCAGCAGTCCGGATGGTGGCTCAGCACT 590  
 QY 560 TCGCACATCATCAGTGTGTTCAAAAACAGATACATACATGTTGGCCAGCTATTTCTGTTG 619  
 DB 591 TTTTTCATCAGCAGGTCTTCCAGGACCGTTCCTGGGGTGATCTTTTCGGCGCTCTTGG 650  
 QY 620 GAAACTTTTACAAGGATTTCTCATCTGTGGTGGTGAAGAGCAGCAATGTGCATCAGC 679  
 DB 651 GAGGTGTCTGCCAGGCTTCTCGTCTCGTGGTGGAGGAGCAACACACTCACCACG 710  
 QY 680 CAGCCACAAATGTTTGGCAGAGCGGAGATCTTGATTTAGTCCATTTCTATGCTACAG 739  
 DB 711 CCGCCCCCAACCTCCACGCGGAGGATCCCGACATTGA--CACCCACCTCTGTTGACCTG 768  
 QY 740 TGGCAGACATCTCAACAATTTATCTCAGGATTTCTGAGTTATGACTCTATTCAGATGCC 799  
 DB 769 GAGTGAGCATGCTTTGGAGATGTTCTCGGATCTCCAGATGAGGAGCTGACCCGCACTG 828

QY 800 AACATGTTCAATGGACATT-----CATGTTACATTCCTCCCG 836  
 DB 829 GTCCGCTTTCATGCTCTGAACACAGACCTGGTTTACTTCCCCATTTCTCTGTTGGCCG 888  
 QY 837 TCTCTCGTGGCTTCTTCAGTCAATCATTTTGTGTAGTCAGATGCCAACTCATTTATTATGA 896  
 DB 889 TCTCTCTGCTGCTCCAGTCCATTTCTTTTGTGCTGCCCTAACGGTCAGGCCCAACAAGCC 948  
 QY 897 CTATTACAGAAAT-----ACTCGGATTTATGAACAGGTTGGTCTCTCTTTGCACCTGGC 950  
 DB 949 CTCGGGCGCGGTGTGCCCATCTCGTTGGTCGAGAGCTGTCGCTTCGGATGCACCTGAC 1008  
 QY 951 TTGGTCAATGGGTCAATTTG---ATTTCCTACCCGATTTGTCACACTAGAATAATGTTCTT 1007  
 DB 1009 CTGGTACCTCGCCACCATGTTCTGTTTCATCAAGGATCCGCTCAACATGCTGGTGTACTT 1068  
 QY 1008 CPTTGTTCATCATCTTTGAGGTTTCCCTGCTCTCATGTAGTTACTTTCAATCATTA 1067  
 DB 1069 TTTGGTGTGCGAGCGGTGTGCGGAACTTTGTTGGCGATCGTGTCTCGCTCAACCAACA 1128  
 QY 1068 TTCAGTGGAGAAAGTTTGCATTTGAGCTCGAACATCATGTCAAATTTACGCTTGTCTTCAAAT 1127  
 DB 1129 CGGTATGCTGTGATCTCGAAGGAGGCGGTGATATGATTTCTTCACGAGACGAT 1188  
 QY 1128 CATGACCACAAGAAATATGAGACCTGGAAGATTTCATTTGAGTGGTTTGGGAGGCTCTTAA 1187  
 DB 1189 CATCACGGTCTGTGATGTCCACCCGGTCTATTGTCACACTGGTTCACGGTGGATTGAA 1248  
 QY 1188 CTATCAGATTGAGCACCATCTTTTCCCAAGATGCCACGACACAACTTTGAACACTGTAT 1247  
 DB 1249 CTATCAGATCGAGCACCACTTTGTTCCCTTCGATGCTCGCCCAACAACCTTTTCAAGATCCA 1308  
 QY 1248 GCCACTGTGTTAA 1260  
 DB 1309 GCCTGCTGTCGAG 1321  
 RESULT 12  
 AAV63638  
 ID AAV63638 standard; cDNA; 655 BP.  
 XX  
 AC AAV63638;  
 XX  
 DT 15-FEB-1999 (first entry)  
 XX  
 DE Contig 2153526 encoding a human desaturase enzyme.  
 XX  
 KW Fatty acid; desaturase; polyunsaturated fatty acid;  
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 KW cholesterol level; endometriosis; premenstrual syndrome; human;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9846763-A1.  
 XX  
 PD 22-OCT-1998.  
 XX  
 PF 10-APR-1998; 98WO-US07126.  
 XX  
 PF 11-APR-1997; 97US-0834655.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 PA (CALJ ) CALGENE LLC.  
 XX  
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
 PI Thurmond J;  
 XX  
 DR WPI; 1998-594582/50.  
 DR P-PSDB; AAW84151.  
 XX



xx DE Contig 2153526 encoding a desaturase enzyme.

xx DE Fatty acid; desaturase; polyunsaturated fatty acid;

xx KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

xx KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

xx KW cholesterol level; endometriosis; premenstrual syndrome;

xx KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;

xx KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

xx OS Homo sapiens.

xx KW W09846765-A1.

xx PN 22-OCT-1998.

xx PD 10-APR-1998; 98WO-US07422.

xx PF 11-APR-1997; 97US-0833610.

xx PR (ABBO ) ABBOTT LAB.

xx PA (CALJ ) CALGENE LLC.

xx PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;

xx PI Thurmond J;

xx PI WPI; 1999-009334/01.

xx DR P-PSDB; AAW85130.

xx DR

xx XX New nucleic acid encoding delta5 and other desaturase enzymes -

xx PT useful in production of oils of increased arachidonic acid content,

xx PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics

xx XX Claim 86; Pages 107-108; 153pp; English.

xx XX The present sequence encodes a human desaturase enzyme. The enzyme

xx CC sequence is used in the methods of the invention. The specification

xx CC describes methods for desaturating a fatty acid and for producing a

xx CC desaturated fatty acid by expressing increased levels of a desaturase.

xx CC The enzyme can be used for desaturating fatty acids. The enzyme can be

xx CC used to produce polyunsaturated fatty acids, which can be used for

xx CC treating malnutrition, in pharmaceutical compositions, in cosmetics or

xx CC in animal feed. The polyunsaturated fatty acids can be used for treating

xx CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,

xx CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.

xx CC They can also be used to inhibit platelet aggregation, cause

xx CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel

xx CC wall smooth muscle and fibrous tissue, reduce or prevent

xx CC gastro-intestinal bleeding and other side effects caused by non-steroidal

xx CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual

xx CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after

xx CC viral infections, treat AIDS, multiple sclerosis, acute respiratory

xx CC syndrome, hypertension and inflammatory skin disorders.

xx XX Sequence 655 BP; 161 A; 181 C; 157 G; 156 T; 0 other;

xx SQ

RESULT 15

AAA49934

ID AAA49934 standard; cDNA; 655 BP.

xx AC AAA49934;

xx AC AAA49934;

xx DT 10-OCT-2000 (first entry)

xx DE Human delta-5-desaturase-related contig 2153526.

xx KW Delta-5-desaturase; human; polyunsaturated fatty acid;

xx KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;

xx KW docosahexaenoic acid; nutrition; feedstuff; ss.

xx OS Homo sapiens.

xx KW W0200040705-A2.

xx PN 13-JUL-2000.

xx PD 29-DEC-1999; 99WO-US31163.

xx PF 08-JAN-1999; 99US-0227613.

xx PR (ABBO ) ABBOTT LAB.

xx PA Mukerji P, Leonard AEY, Huang Y, Parker-Barnes JM;

xx PI WPI; 2000-465975/40.

xx DR

xx XX New polypeptide useful for preparation of nutritional supplements based

xx PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids

xx PT at carbon 5 -

xx XX Example 1; Fig 3; 127pp; English.

xx XX The present sequence is that of contig 2153526, isolated from the

xx CC Inyte Lifeseq database on the basis of homology to Mortierella

xx CC alpina delta-5-desaturase and delta-6-desaturase cDNA sequences.

xx CC A full-length cDNA (see AAA49932) for human delta-5-desaturase (see

xx CC AAY95445) was subsequently obtained. Delta-5-desaturase catalyzes

xx CC the conversion of dihomogamma-linolenic acid to arachidonic acid

xx CC and of 20:4n-3 to eicosapentaenoic acid. Recombinant enzyme,

xx CC expressed in prokaryotic or eukaryotic hosts using the isolated

xx CC human delta-5-desaturase cDNA, can be used in the production of

xx CC polyunsaturated fatty acids that may be added to nutritional,

xx CC veterinary and pharmaceutical compositions.

xx SQ Sequence 655 BP; 161 A; 181 C; 157 G; 156 T; 0 other;

Query Match 4.3%; Score 62.4; DB 21; Length 655;

Best Local Similarity 59.7%; Pred. No. 1.2e-06;

Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1123 CAAATCATGACCAAGAAATATGAGACCTGGAGATTTCATTGCTGCTTTGGGGAGGT 1182

Db 176 CAGCTCCAGGCCACATGCAATGCCAAGTCTCCATGCTGCTTCAATGCTGCTGAGAC 235

QY 1183 CTTAACTATCAGATTGAGCACCATTCTTTCCCAACGATGCCAGCACACAACTTGAACACT 1242

Db 236 CTCACCTTCAGATTGAGCACCATTCTTTCCCAACGATGCCAGCACACAACTTGAACACT 295

QY 1243 GTTATGCCACTTGTAAAGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCCA 1298

Db 296 GTGGCTCCCTGGTGAGTCTCTTGTGTGCCAAGCATGGCATAGTACCACTGCCAA 351

Search completed: July 2, 2003, 13:38:06

Job time : 361.536 secs



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 13:21:06 ; Search time 2260.92 Seconds  
(without alignments)  
10465.482 Million cell updates/sec

Title: US-09-857-583-1  
Perfect score: 1461  
Sequence: 1 gaatttcaatccctctgg.....tccaaattttacattatcc 1461

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	687.4	47.0	717	13	BJ149425
2	641.4	43.9	643	13	BJ110522
3	633	43.3	649	13	BJ118587
C 4	618.4	42.3	665	13	BJ145121
C 5	617	42.2	661	13	BJ139786
C 6	617	42.2	662	13	BJ130343

C 7	616	42.2	660	13	BJ132419
C 8	616	42.2	661	13	BJ154980
C 9	616	42.2	674	13	BJ146307
C 10	615	42.1	656	13	BJ156149
C 11	615	42.1	659	13	BJ145290
C 12	614	42.0	658	13	BJ132385
C 13	613.4	42.0	660	13	BJ148253
C 14	613	42.0	677	13	BJ133013
C 15	612	41.9	656	13	BJ140489
C 16	611.4	41.8	659	13	BJ147839
C 17	611.2	41.8	660	9	AU213515
C 18	611	41.8	654	13	BJ140340
C 19	611	41.8	655	13	BJ138257
C 20	610.2	41.8	659	9	AU213354
21	607	41.5	629	13	BJ112369
22	606	41.5	637	13	BJ112079
23	605.8	41.5	609	9	AU201931
24	604.4	41.4	631	13	BJ126619
C 25	604	41.3	654	13	BJ132022
C 26	602.4	41.2	660	13	BJ146554
27	602	41.2	612	13	BJ102752
28	602	41.2	638	13	BJ119805
29	580	39.7	590	13	BJ127755
30	579.6	39.7	586	13	BJ174196
31	579	39.6	602	13	BJ104762
32	547	37.4	563	13	BJ120819
33	546.4	37.4	548	13	BJ120424
34	546	37.4	568	13	BJ112548
35	541	37.0	563	13	BJ112691
C 36	538.4	36.9	647	13	BJ141242
C 37	535.4	36.6	606	13	BJ140102
38	532.2	36.4	556	13	BJ118832
39	495	33.9	547	13	BJ105378
40	492	33.7	535	13	BJ104402
41	486.8	33.3	672	13	BJ104796
42	485.4	33.2	490	13	BJ117462
43	458.4	31.4	460	9	AU201766
C 44	458.4	31.4	479	13	BJ139830
45	433	29.6	455	13	BJ117633

## ALIGNMENTS

RESULT 1  
BJ149425/c  
LOCUS BJ149425 717 bp mRNA linear EST 24-JAN-2002  
DEFINITION BJ149425 unpublished oligo-capped cDNA library, C. elegans L1 stage  
Caenorhabditis elegans cDNA clone yk1274d04 3', mRNA sequence.  
ACCESSION BJ149425  
VERSION BJ149425.1 GI:18317410  
KEYWORDS EST.  
SOURCE BJ149425.1  
ORGANISM Caenorhabditis elegans.  
Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae  
; Rhabditidae; Peleoderinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 717)  
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
and Sugano,S.  
TITLE A complementary view of the C.elegans genome  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadasi Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.  
Location/Qualifiers  
FEATURES  
source  
1..717  
/organism="Caenorhabditis elegans"  
/strain="N2"  
/db\_xref="taxon:6239"

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/clone="yk1274d04"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      259 a 134 c 142 g 182 t
ORIGIN

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Query Match      47.08; Score 687.4; DB 13; Length 717;
Best Local Similarity 99.9%; Pred. No. 6.9e-157;
Matches 688; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 773 CATGGCTATGACTCTATTCAGATGCGCAACATCTTCATTCGACATTCATCTTACCATTCC 832
DB 717 CGTGGGTTATGACTCTATTCAGATGCGCAACATCTTCATTCGACATTCATCTTACCATTCC 658

QY 833 TCGCTCTCGTGGCTTCTTCAGTCAATCAATTTTGTAGTCTAGATGCCAATCAATATT 892
DB 657 TCGCTCTCGTGGCTTCTTCAGTCAATCAATTTTGTAGTCTAGATGCCAATCAATATT 598

QY 893 ATGACTATTACAGAAATACATGCGATTATGACAGGTTGCTCTCTCTTTCACATGGGCTT 952
DB 597 ATGACTATTACAGAAATACATGCGATTATGACAGGTTGCTCTCTCTTTCACATGGGCTT 538

QY 953 GGTCAATGGTCAATTTGATTTCTTACCCTGATGACAGGTTGCTCTCTCTTTCACATGGGCTT 1012
DB 537 GGTCAATGGTCAATTTGATTTCTTACCCTGATGACAGGTTGCTCTCTCTTTCACATGGGCTT 478

QY 1013 TTCTCATCTGTGTGGAGGTTTCTCTCTCTCATGTAGTACTTCAATCAATATTTCAG 1072
DB 477 TTCTCATCTGTGTGGAGGTTTCTCTCTCTCATGTAGTACTTCAATCAATATTTCAG 418

QY 1073 TGAGAAAGTTTGGATGAGCTGCAACATCATGTCAAAATACGCTTGTCTTCAATCATGA 1132
DB 417 TGAGAAAGTTTGGATGAGCTGCAACATCATGTCAAAATACGCTTGTCTTCAATCATGA 358

QY 1133 CCACAAAGATATGACACCTGGAGATTTCATTCGCTGGCTTGGGAGGCTTAACTATC 1192
DB 357 CCACAAAGATATGACACCTGGAGATTTCATTCGCTGGCTTGGGAGGCTTAACTATC 298

QY 1193 AGATTGAGCACCATTCTTTCCCAACGATGCCAGACACAACTTGAACACTGTTATGCCAC 1252
DB 297 AGATTGAGCACCATTCTTTCCCAACGATGCCAGACACAACTTGAACACTGTTATGCCAC 238

QY 1253 TTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATAACATGGTGGACGATTTTTCACAG 1312
DB 237 TTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATAACATGGTGGACGATTTTTCACAG 178

QY 1313 GATTCCTGGCTTGAATTTGACCAATTCGCAATATTGCAATATTGCTGCTAAATGACTA 1372
DB 177 GATTCCTGGCTTGAATTTGACCAATTCGCAATATTGCAATATTGCTGCTAAATGACTA 118

QY 1373 AAAAGATTGGCTAGATTACCAATTAATCAATTTTATTTTCATGTTCTTATTCGTGGTT 1432
DB 117 AAAAGATTGGCTAGATTACCAATTAATCAATTTTATTTTCATGTTCTTATTCGTGGTT 58

QY 1433 TTAATATTTTCCAAATTTTACCTATTTC 1461
DB 57 TTAATATTTTCCAAATTTTACCTATTTC 29

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RESULT 2
BJ110522
LOCUS
DEFINITION
Caenorhabditis elegans cDNA clone yk113h06 5', mRNA sequence.
ACCESSION
BJ110522

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VERSION          BJ110522.1  GI:18270559
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 643)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome.
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..643
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk113h06"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      212 a 126 c 122 g 183 t
ORIGIN

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Query Match      43.98; Score 641.4; DB 13; Length 643;
Best Local Similarity 99.8%; Pred. No. 1.1e-145;
Matches 642; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 54 AGACAAGAGCATGAGCCATCTTCATTAAATTTGATGAAATGGTGTCAAAATGAGCA 113
DB 1 AGACAAGAGCATGAGCCATCTTCATTAAATTTGATGAAATGGTGTCAAAATGAGCA 60

QY 114 TGCTGTCTCTGAGATCAGATCCAGTGGTGTAGTSCAAATTAACCTATAAAATATGATGATGC 173
DB 61 TGCTGTCTCTGAGATCAGATCCAGTGGTGTAGTSCAAATTAACCTATAAAATATGATGATGC 120

QY 174 CACTACCGTATTCCACACATTCATCTGTTCTAAAGAAGCGTATCAATGGCTGACAGA 233
DB 121 CACTACCGTATTCCACACATTCATCTGTTCTAAAGAAGCGTATCAATGGCTGACAGA 180

QY 234 ATTGAAAAAGAGTGCCCTACACAGAACACAGAGATCCAGATATTAAGGATGACCAAT 293
DB 181 ATTGAAAAAGAGTGCCCTACACAGAACACAGAGATCCAGATATTAAGGATGACCAAT 240

QY 294 CAAAGGAATTGATGATGTGAACATGGGAACCTTTCAATATTTCTGAGAACGATCTGCCCA 353
DB 241 CAAAGGAATTGATGATGTGAACATGGGAACCTTTCAATATTTCTGAGAACGATCTGCCCA 300

QY 354 AATAAATAAAAGTTTCACTGATCTACGATCGGAGTTCGTCGAGAACGATTTATGGATGG 413
DB 301 AATAAATAAAAGTTTCACTGATCTACGATCGGAGTTCGTCGAGAACGATTTATGGATGG 360

QY 414 ATCTCCTTGTCTTACATTTAGAAAAATCTTGAACATCTTCAAAATCTTTTTCGCAAT 473
DB 361 ATCTCCTTGTCTTACATTTAGAAAAATCTTGAACATCTTCAAAATCTTTTTCGCAAT 420

QY 474 CTACCTTCAATACACACATATTTATCTTCCATCAGCTATTTCTAATGGGAGTTTCGCTGGCA 533
DB 421 CTACCTTCAATACACACATATTTATCTTCCATCAGCTATTTCTAATGGGAGTTTCGCTGGCA 480

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QY 534 ACAATTGGGATGTTAATCCATGAAATCCGACATCATCAGTTGTTCAAAAACAGACTACTA 593  
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 DB 481 ACAATTGGGATGTTAATCCATGAAATCCGACATCATCAGTTGTTCAAAAACAAATACTA 540  
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 QY 594 CAATGATTGGCCAGCTATTTCGTTGGAAACATTTTACAAAGGATTCATCTCGTGGTGG 653  
 |||||  
 DB 541 CAATGATTGGCCAGCTATTTCGTTGGAAACATTTTACAAAGGATTCATCTCGTGGTGG 600  
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 QY 654 GAAAGAGCAGCAATGTCATCAGCCAGCCAGCAATGTTGTT 696  
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 DB 601 GAAAGAGCAGCAATGTCATCAGCCAGCCAGCAATGTTGTT 643  
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## RESULT 3

BJ118587  
 LOCUS 649 bp mRNA linear EST 23-JAN-2002  
 DEFINITION BJ118587 unpublished oligo-capped cDNA library, C. elegans L1 stage  
 Caenorhabditis elegans cDNA clone yk1231e10 5', mRNA sequence.

## ACCESSION

BJ118587

## VERSION

EST.

## KEYWORDS

Caenorhabditis elegans.

## ORGANISM

Caenorhabditis elegans

## REFERENCE

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoida

## AUTHORS

1 (bases 1 to 649)  
 Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
 and Sugano,S.

## TITLE

A complementary view of the C.elegans genome

## JOURNAL

Unpublished (2002)

## COMMENT

Contact: Tadasu Shin-I  
 Center For Genetic Resource Information.  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp.

## FEATURES

Location/Qualifiers

1..649

/organism="Caenorhabditis elegans"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1231e10"

/clone\_lib="unpublished oligo-capped cDNA library, C.

elegans L1 stage"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/note="The AD-wrmcDNA library was generated with poly(A)+

RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

BASE COUNT 212 a 129 c 119 g 189 t

## ORIGIN

Query Match 43.3%; Score 633; DB 13; Length 649;

Best Local Similarity 100.0%; Pred. No. 1.2e-143;

Matches 633; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTTTCAATCTCTGGTCCACCGCTGTATCAAAATGGTATTACGAGACAA 60

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DB 17 GAATTTTCAATCTCTGGTCCACCGCTGTATCAAAATGGTATTACGAGACAA 76

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QY 61 GAGCATGAGCCATTTCTTCAATTAATTTGATGAAATGGTGTCAAAATGACCATGCTGTC 120

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DB 77 GAGCATGAGCCATTTCTTCAATTAATTTGATGAAATGGTGTCAAAATGACCATGCTGTC 136

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QY 121 CTGAGATCACATCCAGGTGGTGTGCAATTACTATATAAAATATGATGCCATACC 180

|||||

DB 137 CTGAGATCACATCCAGGTGGTGTGCAATTACTATATAAAATATGATGCCATACC 196

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QY 181 GTATTTCCACATTCCTACTGTTTCTTAAAGAAGCGTATCAATGGCTGACAGATTGAA 240

DB 197 GTATTTCCACATTCCTACTGTTCTTAAAGAAGCGTATCAATGGCTGACAGAAATTGAA 256  
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 QY 241 AAAGAGTGGCCCTACACAAGAACCCAGAGATCCAGATATTAAAGGATGACCCCAATCAAAGGA 300  
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 DB 257 AAAGAGTGGCCCTACACAAGAACCCAGAGATCCAGATATTAAAGGATGACCCCAATCAAAGGA 316  
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 QY 301 ATTGATGATGTGAACATGGGAACCTTTCATATTTCGAGAAACGATCTGCCCAATTAAT 360  
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 DB 317 ATTGATGATGTGAACATGGGAACCTTTCATATTTCGAGAAACGATCTGCCCAATTAAT 376  
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 QY 361 AAAAGTTTCACTGATCTAGTCATGCGAGTTCGTCGAGAAGCACTTATGGATGGATCTCCT 420  
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 DB 377 AAAAGTTTCACTGATCTAGTCATGCGAGTTCGTCGAGAAGCACTTATGGATGGATCTCCT 436  
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 QY 421 TTGTTCTACATTAGAAAAATTTCTTGAACAATCTTCACAAATCTTTTTCGATCTTACCTT 480  
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 DB 437 TTGTTCTACATTAGAAAAATTTCTTGAACAATCTTCACAAATCTTTTTCGATCTTACCTT 496  
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 QY 481 CAATACCACACATATTATCTTCCATCAGCTATTCTTAATGGGAGTTGCGTGCCACAAATTG 540  
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 DB 497 CAATACCACACATATTATCTTCCATCAGCTATTCTTAATGGGAGTTGCGTGCCACAAATTG 556  
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 QY 541 GGATGGTTAATCCATCAATTCGCACATCATCAGTTGTTCAAAAACAGATACTACAATGAT 600  
 |||||  
 DB 557 GGATGGTTAATCCATCAATTCGCACATCATCAGTTGTTCAAAAACAGATACTACAATGAT 616  
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 QY 601 TTGGCCAGCAGTATTTCGTTGGAACATTTTACAA 633  
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 DB 617 TTGGCCAGCAGTATTTCGTTGGAACATTTTACAA 649  
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## RESULT 4

BJ145121/c

## LOCUS

665 bp mRNA linear EST 23-JAN-2002

## DEFINITION

BJ145121 unpublished oligo-capped cDNA library, C. elegans L1 stage

## ACCESSION

BJ145121

## VERSION

EST.

## KEYWORDS

Caenorhabditis elegans.

## ORGANISM

Caenorhabditis elegans

## REFERENCE

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoida

## AUTHORS

1 (bases 1 to 665)  
 Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
 and Sugano,S.

## TITLE

A complementary view of the C.elegans genome

## JOURNAL

Unpublished (2002)

## COMMENT

Contact: Tadasu Shin-I  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp.

## FEATURES

Location/Qualifiers

1..665

/organism="Caenorhabditis elegans"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1215b01"

/clone\_lib="unpublished oligo-capped cDNA library, C.

elegans L1 stage"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/note="The AD-wrmcDNA library was generated with poly(A)+

RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

BASE COUNT 244 a 123 c 126 g 171 t 1 others

## ORIGIN

Query Match 42.3%; Score 618.4; DB 13; Length 665;  
 Best Local Similarity 99.8%; Pred. No. 4.5e-140;  
 Matches 619; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 842 CGTGGCTCTTCAGTCAATCATTTTCTAGTCAGATGCCAATCATATATGACATATT 901  
 DB 665 CGTGGCTCTTCAGTCAATCATTTTCTAGTCAGATGCCAATCATATATGACATATT 606  
 QY 902 ACAGAAATAGTGGGATTTATGAACAGGTTGGTCTCTTTGGCACTGGGCTGGTCAATTGG 961  
 DB 605 ACAGAAATAGTGGGATTTATGAACAGGTTGGTCTCTTTGGCACTGGGCTGGTCAATTGG 546  
 QY 962 GTCAATGTATTTCTACCGATTTGTCAACTAGAAATATGTTCTCTTTCTCTCATC 1021  
 DB 545 GTCAATGTATTTCTACCGATTTGTCAACTAGAAATATGTTCTCTTTCTCTCATC 486  
 QY 1022 TTCTTGGAGGTTTCCCTGCTCTCTCATGTAGTACTTTCAATCATATTCAGTGAGAGT 1081  
 DB 485 TTCTTGGAGGTTTCCCTGCTCTCTCATGTAGTACTTTCAATCATATTCAGTGAGAGT 426  
 QY 1082 TTGCATTGAGCTCGAATCATGTCAATACGTTTCTTCAATCATGACCAACAAGAA 1141  
 DB 425 TTGCATTGAGCTCGAATCATGTCAATACGTTTCTTCAATCATGACCAACAAGAA 366  
 QY 1142 ATATGAGACCTGGAAGATTCATTGACTGGGTTTGGGAGGTCCTTAATCATCATGAGC 1201  
 DB 365 ATATGAGACTTGAAGATTCATTGACTGGGTTTGGGAGGTCCTTAATCATCATGAGC 306  
 QY 1202 ACCATCTTTTCCCAACGATGCCAGACACACTTGAACACTGTTTATGCCCTTCTTAAGG 1261  
 DB 305 ACCATCTTTTCCCAACGATGCCAGACACACTTGAACACTGTTTATGCCCTTCTTAAGG 246  
 QY 1262 AGTTGACGACGAAATGGTTTACCATACATGTCGACGATTTATTCACAGGATTCGCG 1321  
 DB 245 AGTTGACGACGAAATGGTTTACCATACATGTCGACGATTTATTCACAGGATTCGCG 186  
 QY 1322 TTGAATTTGACCAATTCGAAATATTCGAAATGTTGCTGCTAAATTCACATGACATGATG 1381  
 DB 185 TTGAATTTGACCAATTCGAAATATTCGAAATGTTGCTGCTAAATTCACATGACATGATG 126  
 QY 1382 CCTAGATTAGCAATTAATTAATTTATTTTCAATGTTCTATTCGTTGTTTAAATATT 1441  
 DB 125 CCTAGATTAGCAATTAATTAATTTATTTTCAATGTTCTATTCGTTGTTTAAATATT 66  
 QY 1442 TCCAAATTTTACCTATTCC 1461  
 DB 65 TCCAAATTTTACCTATTCC 46

## RESULT 5

BJ139786/c

LOCUS

DEFINITION BJ139786 unpublished oligo-capped cDNA library, C. elegans L1 stage  
 Caenorhabditis elegans cDNA clone yk1150g03 3', mRNA sequence.

ACCESSION BJ139786

VERSION BJ139786.1 GI:18299952

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM

Caenorhabditis elegans.  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea  
 ; Rhabditidae; Pelodierinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 661)

AUTHORS Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.

TITLE A complementary view of the C. elegans genome

JOURNAL Unpublished (2002)

COMMENT Contact: Tadasi Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

Location/Qualifiers

1. 661

## FEATURES

source

/organism="Caenorhabditis elegans"  
 /strain="N2"  
 /db\_xref="taxon:6239"  
 /clone\_lib="yk1150g03"  
 /elegant\_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"  
 /sex="hermaphrodite"  
 /tissue\_type="whole animal"  
 /dev\_stage="L1"  
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPCR8"

BASE COUNT 241 a 122 c 126 g 171 t

ORIGIN

Query Match 42.2%; Score 617; DB 13; Length 661;

Best Local Similarity 100.0%; Pred. No. 9.8e-140;

Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 845 GGCTTCTTCAGTCAATCATTTTGTAGTCAGATGCCAATCATATATGACTATTACA 904  
 DB 661 GGCTTCTTCAGTCAATCATTTTGTAGTCAGATGCCAATCATATATGACTATTACA 602  
 QY 905 GAAATACCTGCGATTTATGAACAGGTTGGTCTCTTTGCACCTGGGCTTGGTCAATGGGTC 964  
 DB 601 GAAATACCTGCGATTTATGAACAGGTTGGTCTCTTTGCACCTGGGCTTGGTCAATGGGTC 542  
 QY 965 AATTGTATTTCTACCGATTTGTCAACTAGAAATATGTTCTCTTTCTCTCATCTTTG 1024  
 DB 541 AATTGTATTTCTACCGATTTGTCAACTAGAAATATGTTCTCTTTCTCTCATCTTTG 482  
 QY 1025 TTGGAGGTTTCTCTCTCTCATGTAGTACTTTCAATCATTTTCACTGAGGAGGTTTG 1084  
 DB 481 TTGGAGGTTTCTCTCTCTCATGTAGTACTTTCAATCATTTTCACTGAGGAGGTTTG 422  
 QY 1085 CATTCAGCTCGAATCATATGTCAAATACGCTTGTCTTCAATCATGACCAACAAGATA 1144  
 DB 421 CATTCAGCTCGAATCATATGTCAAATACGCTTGTCTTCAATCATGACCAACAAGATA 362  
 QY 1145 TGAGACCTGGAAGATTCATTGACTGGGCTTTGGGAGGCTTAACTATCATGATTGAGCACC 1204  
 DB 361 TGAGACCTGGAAGATTCATTGACTGGGCTTTGGGAGGCTTAACTATCATGATTGAGCACC 302  
 QY 1205 ATCTTTTCCCAACGATGCCAGACACACTTGAACACTGTTATGCACCTGTTTAAAGGAGT 1264  
 DB 301 ATCTTTTCCCAACGATGCCAGACACACTTGAACACTGTTATGCCACTTGTTAAGGAGT 242  
 QY 1265 TTGCAGCAGCAAAATGGTTTACCATACATGTCGACGATTTATTCACAGGATTCGCTTG 1324  
 DB 241 TTGCAGCAGCAAAATGGTTTACCATACATGTCGACGATTTATTCACAGGATTCGCTTG 182  
 QY 1325 AAATTGAGCAATTCGGAATATTCGAAATGTTGCTGCTAAATTTGACTATAAAGATTCGCT 1384  
 DB 181 AAATTGAGCAATTCGGAATATTCGAAATGTTGCTGCTAAATTTGACTATAAAGATTCGCT 122  
 QY 1385 AGATTACGATTAATTAATCAATTTATTTTCATGTTCTATTCGTTGTTTAAATATTTTCC 1444  
 DB 121 AGATTACGATTAATTAATCAATTTATTTTCATGTTCTATTCGTTGTTTAAATATTTTCC 62  
 QY 1445 AAATTTTACCTATTCC 1461  
 DB 61 AAATTTTACCTATTCC 45

RESULT 6

BJ130343/c

LOCUS

BJ130343

662 bp

mRNA

linear

EST 23-JAN-2002

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DEFINITION BJ130343 unpublished oligo-capped cDNA library, C. elegans L1 stage
ACCESSION Caenorhabditis elegans cDNA clone yk1042c09 3', mRNA sequence.
VERSION BJ130343.1 GI:18290500
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS ; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 662)
Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
    source
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            /organism="Caenorhabditis elegans"
            /strain="N2"
            /db_xref="taxon:6239"
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            elegans L1 stage"
            /sex="hermaphrodite"
            /tissue_type="whole animal"
            /dev_stage="L1"
            /note="The AD-wrmcDNA library was generated with poly(A)+
            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"
BASE COUNT 242 a 122 c 126 g 171 t 1 others
ORIGIN
Query Match 42.2%; Score 617; DB 13; Length 662;
Best Local Similarity 100.0%; Pred. No. 9.8e-140;
Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 845 GGCTCTCTCAGTCAATCAATTTTGTAGTCAGATGCCCACTCAATATTATGACTATTACA 904
DB 662 GGCTCTCTCAGTCAATCAATTTTGTAGTCAGATGCCCACTCAATATTATGACTATTACA 603
QY 905 GAAATACCTGCGATTATGAACAGGTGGTCTCTCTTTCGACTGGGCTTGGTCATTTGGGTC 964
DB 602 GAAATACCTGCGATTATGAACAGGTGGTCTCTCTTTCGACTGGGCTTGGTCATTTGGGTC 543
QY 965 AATTGTATTTCTACCCGATTGGTCAACTAGATAATGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1024
DB 542 AATTGTATTTCTACCCGATTGGTCAACTAGATAATGTCTCTCTCTCTCTCTCTCTCTCTCTCT 483
QY 1025 TTGGAGGTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1084
DB 482 TTGGAGGTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 423
QY 1085 CATTGAGCTCGAATCATGTCAATTTAGCTTGTCTTCAATCATGACCAAGAAATA 1144
DB 422 CATTGAGCTCGAATCATGTCAATTTAGCTTGTCTTCAATCATGACCAAGAAATA 363
QY 1145 TGAGACCTTGAAGATTCAATTCAGTGGCTTTTGGGAGGTCTTAACATATCAGATTGAGCACC 1204
DB 362 TGAGACCTTGAAGATTCAATTCAGTGGCTTTTGGGAGGTCTTAACATATCAGATTGAGCACC 303
QY 1205 ATCTTTTCCCAACGATGCCAGACACACTTTGAACACTGTTATGCCACTTGTGTAAGGAGT 1264
DB 302 ATCTTTTCCCAACGATGCCAGACACACTTTGAACACTGTTATGCCACTTGTGTAAGGAGT 243
QY 1265 TTGCAGCAGCAATGGTTTACCATACATGGTCGAGGATTATTTACAGAGGATTCGGGCTG 1324

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DB 242 TTGCAGCAGCAATGGTTTACCATACATGGTCGACGATTATTTTCCACAGGATTCGGCTG 183
QY 1325 AAATTGAGCAATTCGAAATATTGCAATATTGCTGCTAAATTAATTAATTAATTAATTAATTA 1384
DB 182 AAATTGAGCAATTCGAAATATTGCAATATTGCTGCTAAATTAATTAATTAATTAATTAATTA 123
QY 1385 AGATTACGATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1444
DB 122 AGATTACGATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 63
QY 1445 AAATTTTACCTATTCC 1461
DB 62 AAATTTTACCTATTCC 46
RESULT 7
BJ132419/c
LOCUS BJ132419
DEFINITION BJ132419 unpublished oligo-capped cDNA library, C. elegans L1 stage
ACCESSION BJ132419
VERSION BJ132419.1 GI:18292576
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS ; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 660)
Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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            /strain="N2"
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            /clone_lib="unpublished oligo-capped cDNA library, C.
            elegans L1 stage"
            /sex="hermaphrodite"
            /tissue_type="whole animal"
            /dev_stage="L1"
            /note="The AD-wrmcDNA library was generated with poly(A)+
            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"
BASE COUNT 242 a 121 c 126 g 171 t
ORIGIN
Query Match 42.2%; Score 616; DB 13; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.7e-139;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 846 GCTTCTTCAGTCAATCAATTTTGTAGTCAGATGCCCACTCAATATTATGACTATTACAG 905
DB 660 GCTTCTTCAGTCAATCAATTTTGTAGTCAGATGCCCACTCAATATTATGACTATTACAG 601
QY 906 AAATACCTGCGATTATGAACAGGTGGTCTCTCTTTCGACTGGGCTTGGTCATTTGGGTCA 965
DB 600 AAATACCTGCGATTATGAACAGGTGGTCTCTCTTTCGACTGGGCTTGGTCATTTGGGTCA 541
QY 966 ATGTATTTCCTTACCAGGATTGGTCAACTAGATAATATGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1025

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/note="The AD-wmcdna library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 242 a 119 c 125 g 171 t 1 others  
ORIGIN

Query Match 42.0%; Score 614; DB 13; Length 658;  
Best Local Similarity 100.0%; Pred. No. 5.2e-139;  
Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 848 TTCTTCAGTCATCATTTTGTAGTCAGATGCCAATCAATTAATTAAGACTATTACAGAA 907
Db 658 TTCTTCAGTCATCATTTTGTAGTCAGATGCCAATCAATTAATTAAGACTATTACAGAA 599
QY 908 ATACTCCGATTTATGAACAGGTGGCTCTCTTTGCACATGGGCTTGGTCAATGGGCAAT 967
Db 598 ATACTCCGATTTATGAACAGGTGGCTCTCTTTGCACATGGGCTTGGTCAATGGGCAAT 539
QY 968 TGTATTTCTACCCGATTTGGTCAACTAGATAAATGTTCTTCCTTTCTTCATCTTGTGG 1027
Db 538 TGTATTTCTACCCGATTTGGTCAACTAGATAAATGTTCTTCCTTTCTTCATCTTGTGG 479
QY 1028 GAGGTTTCTCTCTCTCATGTAGTTACTTTCATCAATTAATTAATTAAGACTATTGCAAT 1087
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QY 1268 CAGCAGCAATGGTTTACCATACATGGTCGACGATTAATTTACAGGATTTCTGGCTTGA 1327
Db 238 CAGCAGCAATGGTTTACCATACATGGTCGACGATTAATTTACAGGATTTCTGGCTTGA 179
QY 1328 TTGACGAATCCGAATATGCAAAATGTTGCTGCTAAATGACTAAAGATTTGCCCTAGA 1387
Db 178 TTGACGAATCCGAATATGCAAAATGTTGCTGCTAAATGACTAAAGATTTGCCCTAGA 119
QY 1388 TTACGATTAATTAATCAATTTATTTTCATGTTCTATTCGTGTTTATATTTTCCAAA 1447
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QY 1448 TTTTACCCTATTCC 1461
Db 58 TTTTACCCTATTCC 45
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RESULT 13  
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LOCUS  
DEFINITION  
Caenorhabditis elegans cDNA clone yk1260f09 3', mRNA sequence.  
ACCESSION  
BJ148253  
VERSION  
1 (bases 1 to 660)  
KEYWORDS  
EST.  
SOURCE  
Caenorhabditis elegans.  
ORGANISM  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae  
; Rhabditidae; Pelodierinae; Caenorhabditis.  
REFERENCE  
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.  
and Sugano, S.  
A complementary view of the C. elegans genome  
TITLE

JOURNAL  
COMMENT

Unpublished (2002)  
Contact: Tadashi Shin-I  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.

FEATURES  
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/dev\_stage="L1"  
/note="The AD-wmcdna library was generated with poly(A)+  
RNA isolated from both hermaphrodite and male N2 worms of  
all larval stages, embryos, adults and dauers and the  
subsequent generation of cDNAs by poly(A) priming. The  
cDNAs were cloned into pPC86"

BASE COUNT 241 a 121 c 126 g 171 t 1 others  
ORIGIN

Query Match 42.0%; Score 613.4; DB 13; Length 660;  
Best Local Similarity 99.7%; Pred. No. 7.4e-139;  
Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 660 GCTTCTTCAGTCATCAATTTTGTAGTCAGATGCCAATCAATTAATTAAGACTATTACAG 601
QY 906 AATACTGCGATTTATGAACAGGTGGCTCTCTTTGCACATGGGCTTGGTCAATGGGTCA 965
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QY 966 ATTGATTTTCTACCCGATTTGGTCAACTAGATAAATGTTCTTCTTCTTCTCATCTTGT 1025
Db 540 ATTGATTTTCTACCCGATTTGGTCAACTAGATAAATGTTCTTCTTCTTCTCATCTTGT 481
QY 1026 TGGAGGTTTCTCTCTCTCATGTAGTTACTTTCAATCAATTAATTAAGACTATTGTC 1085
Db 480 TGGAGGTTTCTCTCTCTCATGTAGTTACTTTCAATCAATTAATTAAGACTATTGTC 421
QY 1086 ATTGAGCTCGAATCATGTCAAAATTAAGCTTGTCTTCAATCATGACCAAGAAATAT 1145
Db 420 ATTGAGCTCGAATCATGTCAAAATTAAGCTTGTCTTCAATCATGACCAAGAAATAT 361
QY 1146 GAGACCTGGAAGATTCATTCAGCTGGCTTTGGGAGGCTTTAACTATCATGATTGAGCACA 1205
Db 360 GAGACCTGGAAGATTCATTCAGCTGGCTTTGGGAGGCTTTAACTATCATGATTGAGCACA 301
QY 1206 TCTTTTCCCAACGATGCCACGACACAACTTTGAACACTGTTATGCCACTTGTAAAGAGTT 1265
Db 300 TCTTTTCCCAACGATGCCACGACACAACTTTGAACACTGTTATGCCACTTGTAAAGAGTT 241
QY 1266 TGCAGCAGCAATTTGGTTTACCATACATGTCGAGGATTAATTTACAGAGATTTCTGGCTGA 1325
Db 240 TGCAGCAGCAATTTGGTTTACCATACATGTCGAGGATTAATTTACAGAGATTTCTGGCTGA 181
QY 1326 AATTGAGCAATTCGGAATATTTCAAAATGTTGCTGCTAAATTTGACTAAAAGATTTGCTA 1385
Db 180 AATTGAGCAATTCGGAATATTTCAAAATGTTGCTGCTAAATTTGACTAAAAGATTTGCTA 121
QY 1386 GATTACGATTAATTAATCAATTTATTTTCTATGTTTCTTATTCGTTGTTTATATTTTCCA 1445
Db 120 GATTACGATTAATTAATCAATTTATTTTCTATGTTTCTTATTCGTTGTTTATATTTTCCA 61
QY 1446 AATTTTACCCTATTCC 1461
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Db      60 AATTTTACCTATTCC 45

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LOCUS    BJ133013 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION
ACCESSION BJ133013
VERSION   BJ133013.1 GI:18293170
KEYWORDS EST.
SOURCE    Caenorhabditis elegans.
ORGANISM  Caenorhabditis elegans.
          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
          ; Rhabditidae; Peloderinae; Caenorhabditis.
          1 (bases 1 to 677)
REFERENCE Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
          and Sugano,S.
          A complementary view of the C.elegans genome
          Unpublished (2002)
          Contact: Tadasu Shin-I
          Center For Genetic Resource Information
          National Institute of Genetics
          1111 Yata, Mishima, Shizuoka 411-8540, Japan
          Tel: 81-559-81-6856
          Fax: 81-559-81-6855
          Email: tshini@genes.nig.ac.jp.
          Location/Qualifiers
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            /tissue_type="whole animal"
            /dev_stage="L1"
            /note="The AD-wrmcDNA library was generated with poly(A)+
            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"

FEATURES
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Query Match 42.0%; Score 613; DB 13; Length 677;
Best Local Similarity 100.0%; Pred. No. 9.2e-139;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      |
Qy 909 TACTGCGATTATGAACAGTTGGTCTCTCTTCACGTCGGCTGGTCATTTGGGTCATT 968
Db      |
Qy 617 TACTGCGATTATGAACAGTTGGTCTCTCTTCACGTCGGCTGGTCATTTGGGTCAAAT 558
Db      |
Qy 969 GTATTTCTACCCGATTTGGTCAACTAGAAATATGTTCTCTCTCTCTCTCTCTCTCTCT 1028
Db      |
Qy 557 GTATTTCTACCCGATTTGGTCAACTAGAAATATGTTCTCTCTCTCTCTCTCTCTCTCT 498
Db      |
Qy 1029 AGGTTTCTGCTCTCTCATGATGATCTTTCAATCATTTATTCAGTGGAGAAAGTTTGCATT 1088
Db      |
Qy 497 AGGTTTCTGCTCTCTCATGATGATCTTTCAATCATTTATTCAGTGGAGAAAGTTTGCATT 438
Db      |
Qy 1089 GAGTCGCAACATCATGTCAAATATGCTTCTTCAAATCATGACCAACAAATATATGAG 1148
Db      |
Qy 437 GAGTCGCAACATCATGTCAAATATGCTTCTTCAAATCATGACCAACAAATATATGAG 378
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Qy 1149 ACCTGGAAGATTCAATGACTGGCTTTGGGAGGCTTAACTATCATCATGATTTGAGCACCATCT 1208
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Qy 377 ACCTGGAAGATTCAATGACTGGCTTTGGGAGGCTTAACTATCATCATGATTTGAGCACCATCT 318

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Qy 1269 AGCAGCAATAGTTTACCATATCATGTCGACGATTTATTCACAGGATTTCTGCTTTGAAAT 1328
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Qy 1329 TGAGCAATTCGAAATATTTGCAATGTTGCTGCTAAATGACTAAAAGATTTGCCTAGAT 1388
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Qy 137 TACGATTAATTAACAATTTATTTTCATGTTCTTATTCGTTGCTTTTAAATATTTTCCAAAT 78
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RESULT 15
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DEFINITION
ACCESSION BJ140489
VERSION   BJ140489.1 GI:18300655
KEYWORDS EST.
SOURCE    Caenorhabditis elegans.
ORGANISM  Caenorhabditis elegans.
          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
          ; Rhabditidae; Peloderinae; Caenorhabditis.
          1 (bases 1 to 656)
REFERENCE Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
          and Sugano,S.
          A complementary view of the C.elegans genome
          Unpublished (2002)
          Contact: Tadasu Shin-I
          Center For Genetic Resource Information
          National Institute of Genetics
          1111 Yata, Mishima, Shizuoka 411-8540, Japan
          Tel: 81-559-81-6856
          Fax: 81-559-81-6855
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            /tissue_type="whole animal"
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            RNA isolated from both hermaphrodite and male N2 worms of
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BASE COUNT 240 a 120 c 125 g 171 t
ORIGIN

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QY 1030 GGTTCCTGCTCTCATCTAGTACTTCAATCATATTCACTGGAGAGTTTGCATTG 1089  
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QY 476 GGTTCCTGCTCTCATCTAGTACTTCAATCATATTCACTGGAGAGTTTGCATTG 417  
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QY 1090 ACCTCGAATCATGTCRAATACGCTTCTTCAATCATGACCAACAAGAAATATGAGA 1149  
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QY 356 CTTGGAAGATTCAATGACTGGCTTTGGGGAGGTCTTAACTATCAGATTGAGCACCACATCTT 297  
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QY 296 TTCCCAACGATGCCAGCACAACTTGAACACTGTTATGCCACTTCTTAAGGAGTTTGA 237  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 236 GCAGCAATGGTTTACCATACATGGTCGACGATTATTTACAGGATTCTGGCTTGAATT 177  
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QY 1330 GAGCAATTCCGAAATATTGCAATGTTGCTGCTAAATTGACTAAAAAGATTGCTAGATT 1389  
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QY 176 GAGCAATTCCGAAATATTGCAATGTTGCTGCTAAATTGACTAAAAAGATTGCTAGATT 117  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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QY 116 ACGATTAAATCAATTTATTTTCAATGTTCTATTCGTTGTTTAAATATTTTCCAAATT 57  
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GenCore version 5.1.6  
Copyright (C) 1993 - 2003 CompuGen Ltd.

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	629	25.8	457	4	US-09-330-235-18
6	629	25.8	458	4	US-09-439-261-10
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8	629	25.8	458	4	US-09-227-613-11
9	629	25.8	458	4	US-09-227-613-41
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14	555	22.8	355	4	US-09-363-574-5
15	555	22.8	355	4	US-09-363-526-5
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19	408.5	16.8	432	4	US-09-227-613-9
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25	403.5	16.6	448	1	US-08-789-936-5
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31	396	16.3	444	4	US-09-439-261-43	Sequence 43, Appl
32	396	16.3	444	4	US-09-227-613-42	Sequence 42, Appl
33	387	15.9	452	4	US-08-934-254-27	Sequence 27, Appl
34	311	12.8	356	4	US-09-439-261-19	Sequence 19, Appl
35	311	12.8	356	4	US-09-227-613-18	Sequence 18, Appl
36	298.5	12.3	287	4	US-09-439-261-13	Sequence 13, Appl
37	298.5	12.3	287	4	US-09-227-613-14	Sequence 14, Appl
38	298.5	12.3	288	4	US-09-439-261-14	Sequence 14, Appl
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41	298.5	12.3	288	4	US-09-227-613-15	Sequence 15, Appl
42	284.5	11.7	87	2	US-08-834-655-10	Sequence 10, Appl
43	284.5	11.7	87	3	US-08-834-033A-11	Sequence 11, Appl
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45	284.5	11.7	87	4	US-09-363-526-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-08-834-655-2  
; Sequence 2, Application US/08834655  
; Patent No. 5968809  
; GENERAL INFORMATION:  
; APPLICANT: KNUTZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,655  
; FILING DATE: 11-APR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RAE-VENTER, BARBARA  
; REGISTRATION NUMBER: 32,750  
; REFERENCE/DOCKET NUMBER: CGNE.124.0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 328-4400  
; TELEFAX: (650) 328-4477  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 457 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-834-655-2

Query Match 25.8%; Score 629; DB 2; Length 457;  
Best Local Similarity 33.0%; Pred. No. 1.1e-54;  
Matches 134; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY	4	REQEHEFFFKIDCKWCQCIDDAVLRSHPGGSAITYYKNMDATTVTHHTHTSGKEAYQWLT	63
Db	25	KKDAEAPFLMIIDKNKYVDVREFV-PDHGGSVILTHVGKDGDTGDTFTH---PEA-AWET	79
QY	64	ELAKCECTQBPEDIPDKDDPIKGIDDDVNGMTFNISEKRSQAINKSFTDLRMVRVAREGLMD	123
Db	80	LANFYVGDIDESDDRIKNDDE-----AAEVRK-----LRLTFLQSLGYD	118
QY	124	GSPLFYTRKI-----LETIFTILPFIYLOYHTY-YLPSAILMGVAQOGLWLIHBEFAHHQ	177
Db	119	SSKAYYAFKVSFNLCINGLSVTIVAKWGQSTLANVLSSAALLGLEFWQCGWLAHDFLHHQ	178
QY	178	LFKNRYNDLASYFVGNFLOQSGGKKEQHNHHAATNYNDLVNVRGCDGLDLVPFYATVAEHL	237
Db	179	VFODRFMGDDLFGAELGGVCQGSSSWNKDKRHTHAAPNVIGEDPDIDITHPL-LTWSEHA	237
QY	238	NNYSQD-----SNVMTLFRQHVHTFF--MLPFLRLSWLQSIIFY-----SQ	278
Db	238	LEMFSDDVDEELTRMWSRFMVLNQTWFYFPILSFARLSWCQLQSILFVLPGNAHKPSGAR	297
QY	279	MPHYHYDYRNTAIYEQVGLSLHWAWSLGQLY-FLPDWSTRIIMFPLVSHLVGCGFLLSHVV	337
Db	298	VP-----ISLVEQLSLAMHHTWYLATMFLFKDPVNNMLVFLVSQAVCGNLLAIYF	348
QY	338	TFNHYSYEKFPALSSNIMSNTACLOIMTTRNRMPGRFIDWLWGGLNQYIEHHLFTPTMPRN	397
Db	349	SLNHNGMPVLSKEBAVDMDFTKQIITGRDVPHGLFANWFVGGNLNQYIEHHLFPPSPMRHN	408
QY	398	LNTVMPVLVBKFAAANGLPYVYDDYFTGFWMLEIOEFNRNIANYAAKITK	444
Db	409	FSKIQAIVETLCKKYNRYHTTGMIETGAEYFSLNEVYSKAASKMGK	455

## RESULT 2

US-0834-033A-2  
Sequence 2, Application US/08834033A  
Patent No. 6075183  
GENERAL INFORMATION:  
APPLICANT: KNUITZON, DEBORAH  
APPLICANT: MUKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THURMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834,033A  
FILING DATE: 11-APR-1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-300, USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 457 amino acids

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; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-033A-2

Query Match          25.88; Score 629; DB 3; Length 457;
Best local similarity 33.08; Pred. No. 1.1e-34;
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

Qy      4  RECHPEFFFKIDGKCQIDDAVLRHSGGSAITTKYKNDDATVFHTFGSKEAYQWL 63
Db      25  KKDAEAPFLMIINKYVDREFV-PHPGGSVLTHVGKDGTDVDFTFH---PEA-ANET 79

Qy      64  ELKKECTOPETPIDKDDPIKIGIDDVMGTFNISEKRSQAQINSKFTDLRMRYRAGLMD 123
Db      80  LANFYVGIDIDESDRDKNDDF-----AAEVRK----LRTLFQSLGYD 118

Qy      124  GSPLFYRKI-----LETFTILFAFYQYHTY-YLPSSATLMGVAMQOLGWLTHEPAHQ 177
Db      119  SSKAYAFKVSFNLGSLSTVIAVKGOTSTLANVLSAALGLFWQCGWLHAHDELUHQ 178

Qy      178  LFNRYNYNDLASFVGNFLQSGSGGWKEOHNVHHAATNVVGRDGLDLVPFYATVAEHL 237
Db      179  VFQDRFGWDLFGAFLGCVGCGFSSSWKKDKNTHHAAPNVHGDPDIDTHPL-LTWSEHA 237

Qy      238  NNYSQD-----SWVMTLFRQWVHHTF--MLPFLRLSNLQSIIF-----SQ 278
Db      238  LEMFSVDVPDELRMRMSRFVNLQOTWYFPILSFARLSWCLQSILFLPNQAOKPSSGAR 297

Qy      279  MPYHYDYDYNTAIYEQVGLSLHWANSLGOLY-FLPDWSTRIMEFLVSHLVGGFLSHVV 337
Db      298  VP-----ISLVQSLSAMHWHTYLATMFLFIKDPVNMUWYFLVLSQVCGNLLAIVF 348

Qy      338  TFNHYSEYKFPALSSNTMSNYACIQIATTRNMRPGRITDNLWGLNLTQIEHLEPPTMPRH 397
Db      349  SLNHGMPVLSKEEAVDMDEFTQKITIGRDVHPGLFANFTGGLNLTQIEHLEPSPMRHN 408

Qy      398  LNTVMPVLVKBEAANGLPYVMDDYFTGFWLEIEQGFRIANVAALKTK 444
Db      409  FSKIQAPVETLCKKNYRVYHTTGWIGTAETAEVFSRLNEVSKAASKMGK 455

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### RESULTS

US-09-363-574-2  
 Sequence 2, Application US/09363574  
 Patent No. 6136574  
 GENERAL INFORMATION:  
 APPLICANT: KNUTZON, DEBORAH  
 APPLICANT: MURKERJI, PRADIP  
 APPLICANT: HUANG, YUNG-SHENG  
 APPLICANT: THURMOND, JENNIFER  
 APPLICANT: CHAUDHARY, SUNITA  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
 OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
 STREET: 2001 FERRY BUILDING  
 CITY: SAN FRANCISCO  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/363,574  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-202 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 457 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-363-574-2

Query Match 25.8%; Score 629; DB 4; Length 457;  
Best Local Similarity 33.0%; Pred. No. 1.le-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY 4 ROEHEPPFIKIDGKCQIDDVLRSHPGGSAITTYKNMDATTVFHTGSKAYQWL 63  
DB 25 KKDAEAPFLMIIDNKVYDREFV-PDHPGGSVILTHVGKDGTDVDFTH---PEA-AWET 79  
QY 64 ELKKECPTQEPPIKDDPIKIGDIDVNMGTFFNISEKRSQAQINKSFTDLRMVRAEGLMD 123  
DB 80 LANFYVGDDIDESDRDIKNDDF-----AAEVRK-----LRTLFSLSGYD 118  
QY 124 GSPLFYIRKI-----LETIFTILFAFYLOVHTY-YLPSAILMGVAMQOLGLIHEFAHQ 177  
DB 119 SSKAYFAKVSFNLCTGLSTVIVAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHQ 178  
QY 178 LFNRYNDLASVYGNFLOGSSGQKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237  
DB 179 VFQDFWGLDGLFAGLGGVCGQSSWWKDKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237  
QY 238 NNYSDQ-----SWMTLFRWQHVHTF--MLPFLRLSLWLLQSIIFV-----SQ 278  
DB 238 LEMFSDVPDEELTRMMSRFVNLQNTWFFPILSFARLSWCLQSLFVLPNGQAHKPSGAR 297  
QY 279 MPTHYDYRNTAIYEQVGLSLHWANSLGOLY-FLPDWSTRIMFFLVSHLVGGLLHV 337  
DB 298 VP-----ISLVEQLSLAMHTWYLATMFLFKDPVNMVLYFLVSQAVCNLLAIYF 348  
QY 338 TFNHYVEKFASSNTMSNYACIQIMTRNMRGRFIDMLWGLNTOIEHHLFTPMRHN 397  
DB 349 SLNNGMPVISKEEAVIDMDFETKQIITGRDVHPLGFANFTGGLNYQIEHHLFPPSMRHN 408  
QY 398 LNTVMPLVKEFAAANGLPYVDDYFTGFWLEIEQFRNIANVAALTK 444  
DB 409 FSKIQPAVETLCKKYNVRYHTTGMIETAEVFSRLNEVSKAASKMGK 455

RESULT 4  
US-09-363-526-2  
Sequence 2, Application US/09363526  
Patent No. 6410288  
GENERAL INFORMATION:  
APPLICANT: KNUZON, DEBORAH  
APPLICANT: MURKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THORMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,526  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-201 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 457 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-363-526-2

Query Match 25.8%; Score 629; DB 4; Length 457;  
Best Local Similarity 33.0%; Pred. No. 1.le-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY 4 ROEHEPPFIKIDGKCQIDDVLRSHPGGSAITTYKNMDATTVFHTGSKAYQWL 63  
DB 25 KKDAEAPFLMIIDNKVYDREFV-PDHPGGSVILTHVGKDGTDVDFTH---PEA-AWET 79  
QY 64 ELKKECPTQEPPIKDDPIKIGDIDVNMGTFFNISEKRSQAQINKSFTDLRMVRAEGLMD 123  
DB 80 LANFYVGDDIDESDRDIKNDDF-----AAEVRK-----LRTLFSLSGYD 118  
QY 124 GSPLFYIRKI-----LETIFTILFAFYLOVHTY-YLPSAILMGVAMQOLGLIHEFAHQ 177  
DB 119 SSKAYFAKVSFNLCTGLSTVIVAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHQ 178  
QY 178 LFNRYNDLASVYGNFLOGSSGQKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237  
DB 179 VFQDFWGLDGLFAGLGGVCGQSSWWKDKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237  
QY 238 NNYSDQ-----SWMTLFRWQHVHTF--MLPFLRLSLWLLQSIIFV-----SQ 278  
DB 238 LEMFSDVPDEELTRMMSRFVNLQNTWFFPILSFARLSWCLQSLFVLPNGQAHKPSGAR 297  
QY 279 MPTHYDYRNTAIYEQVGLSLHWANSLGOLY-FLPDWSTRIMFFLVSHLVGGLLHV 337  
DB 298 VP-----ISLVEQLSLAMHTWYLATMFLFKDPVNMVLYFLVSQAVCNLLAIYF 348  
QY 338 TFNHYVEKFASSNTMSNYACIQIMTRNMRGRFIDMLWGLNTOIEHHLFTPMRHN 397  
DB 349 SLNNGMPVISKEEAVIDMDFETKQIITGRDVHPLGFANFTGGLNYQIEHHLFPPSMRHN 408  
QY 398 LNTVMPLVKEFAAANGLPYVDDYFTGFWLEIEQFRNIANVAALTK 444  
DB 409 FSKIQPAVETLCKKYNVRYHTTGMIETAEVFSRLNEVSKAASKMGK 455

RESULT 5  
US-09-330-235-18  
Sequence 18, Application US/09330235  
Patent No. 6459018  
GENERAL INFORMATION:  
APPLICANT: Knutzon, Debbie  
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS  
FILE REFERENCE: MCOO.156.0005  
CURRENT APPLICATION NUMBER: US/09/330,235  
CURRENT FILING DATE: 1999-06-10



; PRIOR APPLICATION NUMBER: 60/089,043  
; PRIOR FILING DATE: 1998-06-12  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 457  
; TYPE: PRT  
; ORGANISM: Mortierella alpina  
US-09-330-235-18

Query Match 25.8%; Score 629; DB 4; Length 457;  
Best Local Similarity 33.0%; Pred. No. 1.1e-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;  
QY 4 REQHEPFIKIDGKWCQIDDAVLRSHPGGSAITTYKKNMDATTVFHTGSKAYQWLT 63  
DB 25 KKDAEAPFLMIIDNKVDVREVF-PDHPGGSVILTHVGKDGTDVDFTFH---PEA-AWET 79  
QY 64 ELKKECPTQEPPIKIDKDDPIKIGIDDDVNMGTFNISEKRSQAINKSFDTLDRMRVRAEGLMD 123  
DB 80 LANFVVGIDIDESDRDKNDPF-----AAEVRK-----LRTLFSGLGYD 118  
QY 124 GSPFYIRKI-----LETIFILFAFYLYQYHTY-YLPSAILMGVAMQQLGLIHEFAHQ 177  
DB 119 SSKAYYAFKVSFNLICWGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGWLAHDFLHQ 178  
QY 178 LFKNRYNDLASVYFVGNFLOGFSSGGWKEQHNHHAATNVVGRDGLDLVPFYATVAEHL 237  
DB 179 VFQDFWGLDFGAFGLGGVCGQFSSWKKDKHNTHAAPNVHGEDPDIDTHPL-LTWSEHA 237  
QY 238 NNYSDQ-----SWMTLFRWQHVVHTF--MLPFLRLSWLLQSIIFV-----SQ 278  
DB 238 LEMSDVPDEELTRWMSRFVNLQTFYFPLSFARLSWCLOSILFVLPNGQAHKPSGAR 297  
QY 279 MPTHYDYRNTAIYEQVGLSLHMAWSLGQLY-FLPDWSTRIEMFVLSHLVGGFLLSHVY 337  
DB 298 VP-----ISLVEQLSLAMHTWYLATMFLFKDPVNMVLYFLVSAQVGNLLAIVF 348  
QY 338 TFNHYSEKFAFSLNSNMSNYACLOIMTTRNMRPGRFDIWLGGGLNYQIEHHLFPTMPRHN 397  
DB 349 SLNHGMPVISKEEAVDMDFTFKQITGRDVHPLGFANWFTGGLNYQIEHHLFPTMPRHN 408  
QY 398 LNTVPLVKEFAAANGLPYWDVDTFTGFWLEIEQFRNIANVAALKTK 444  
DB 409 FSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

## RESULT 6

US-09-439-261-10  
; Sequence 10, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: VARIANT  
; LOCATION: (458)...(458)  
; OTHER INFORMATION: Xaa = Unknown or other at position 458  
US-09-439-261-10

Query Match 25.8%; Score 629; DB 4; Length 458;  
Best Local Similarity 33.0%; Pred. No. 1.1e-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;  
QY 4 REQHEPFIKIDGKWCQIDDAVLRSHPGGSAITTYKKNMDATTVFHTGSKAYQWLT 63  
DB 25 KKDAEAPFLMIIDNKVDVREVF-PDHPGGSVILTHVGKDGTDVDFTFH---PEA-AWET 79  
QY 64 ELKKECPTQEPPIKIDKDDPIKIGIDDDVNMGTFNISEKRSQAINKSFDTLDRMRVRAEGLMD 123  
DB 80 LANFVVGIDIDESDRDKNDPF-----AAEVRK-----LRTLFSGLGYD 118  
QY 124 GSPFYIRKI-----LETIFILFAFYLYQYHTY-YLPSAILMGVAMQQLGLIHEFAHQ 177  
DB 119 SSKAYYAFKVSFNLICWGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGWLAHDFLHQ 178  
QY 178 LFKNRYNDLASVYFVGNFLOGFSSGGWKEQHNHHAATNVVGRDGLDLVPFYATVAEHL 237  
DB 179 VFQDFWGLDFGAFGLGGVCGQFSSWKKDKHNTHAAPNVHGEDPDIDTHPL-LTWSEHA 237  
QY 238 NNYSDQ-----SWMTLFRWQHVVHTF--MLPFLRLSWLLQSIIFV-----SQ 278  
DB 238 LEMSDVPDEELTRWMSRFVNLQTFYFPLSFARLSWCLOSILFVLPNGQAHKPSGAR 297  
QY 279 MPTHYDYRNTAIYEQVGLSLHMAWSLGQLY-FLPDWSTRIEMFVLSHLVGGFLLSHVY 337  
DB 298 VP-----ISLVEQLSLAMHTWYLATMFLFKDPVNMVLYFLVSAQVGNLLAIVF 348  
QY 338 TFNHYSEKFAFSLNSNMSNYACLOIMTTRNMRPGRFDIWLGGGLNYQIEHHLFPTMPRHN 397  
DB 349 SLNHGMPVISKEEAVDMDFTFKQITGRDVHPLGFANWFTGGLNYQIEHHLFPTMPRHN 408  
QY 398 LNTVPLVKEFAAANGLPYWDVDTFTGFWLEIEQFRNIANVAALKTK 444  
DB 409 FSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

## RESULT 7

US-09-439-261-44  
; Sequence 44, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: VARIANT  
; LOCATION: (458)...(458)  
; OTHER INFORMATION: Xaa = Unknown or other at position 458  
US-09-439-261-44

Query Match 25.8%; Score 629; DB 4; Length 458;  
Best Local Similarity 33.0%; Pred. No. 1.1e-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

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QY 4 REOEHEPFIKIDGKCQIDDAVLRSHPGGSAITTYKNMDATVFTHTGSKAEAYQWLT 63
DB 25 KKDAEAPFLMIIDNKVYDREFV-PDHPGGSVILTHVGKDGTDVDFTEH---PEA-AWET 79
QY 64 ELKKECTQEPIDPKDPIKIGDIDVNMGTFNISEKRSQAQINKSFTDLRMVRRAEGLMD 123
DB 80 LANFVYGDIDESDRDIKNDFF-----AAEVRK-----LRTLFSQSLGYD 118
QY 124 GSPFLFYIRKI-----LETITLILFAFYLOYHTY-YLPSSAILMGVAAQGLWLIHEFAHQ 177
DB 119 SSKAYYAFKVSFNLCTWGLSTVIVAKWGQTSTLANVLSAALLGLFWQCCGWLADHFLHQ 178
QY 178 LFKNRYNDLASFYVGNFLQGSFGGKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237
DB 179 VFQDRFWGDLFGAFLGGVCGQFSFSSWKKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237
QY 238 NNYSD-----SWMTLFRWQHVVHTF--MLPFLRLSMLLSQSIIFV-----SQ 278
DB 238 LEMFSDVPDEELTRMSRWFVNLQTFYFPIILSFARLSWCLQSILFVLPNGOAHKPSGAR 297
QY 279 MPTHYDYRYNTAIYEOVGLSLHWASLGQLY-FLPDWSTRIMEFLVSLHVGFLSHVY 337
DB 298 VP-----ISLVEQLSLAMHTWYLATMFLFIKDPVNMVLYFLVSQAACGNLLAIVF 348
QY 338 TPNHYSVEKFAALSSNIMSYACLIQIMTRNMRPGRFIDWLWGLNLYQIEHHLFPTMPRHN 397
DB 349 SLNHGMPVISKEEAVIDMDEFTKQIITGRDVHFGLFANWFTGGLNLYQIEHHLFPTMPRHN 408
QY 398 LNTVMPLVKEFAAANGPLVMVDYFTGFWLEIEQFNRNIANVAALTK 444
DB 409 FSKIQPAVETLCKKYNVRYHTTGMIETGAEVFSRLNEVSKAASKMGK 455
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## RESULT 8

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US-09-227-613-11
; Sequence 11, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradiip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: xaa at position 458 is unknown or other.
US-09-227-613-11
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Query Match 25.8%; Score 629; DB 4; Length 458;  
Best Local Similarity 33.0%; Pred. No. 1.1e-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

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QY 4 REOEHEPFIKIDGKCQIDDAVLRSHPGGSAITTYKNMDATVFTHTGSKAEAYQWLT 63
DB 25 KKDAEAPFLMIIDNKVYDREFV-PDHPGGSVILTHVGKDGTDVDFTEH---PEA-AWET 79
QY 64 ELKKECTQEPIDPKDPIKIGDIDVNMGTFNISEKRSQAQINKSFTDLRMVRRAEGLMD 123
DB 80 LANFVYGDIDESDRDIKNDFF-----AAEVRK-----LRTLFSQSLGYD 118
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QY 124 GSPFLFYIRKI-----LETITLILFAFYLOYHTY-YLPSSAILMGVAAQGLWLIHEFAHQ 177
DB 119 SSKAYYAFKVSFNLCTWGLSTVIVAKWGQTSTLANVLSAALLGLFWQCCGWLADHFLHQ 178
QY 178 LFKNRYNDLASFYVGNFLQGSFGGKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237
DB 179 VFQDRFWGDLFGAFLGGVCGQFSFSSWKKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237
QY 238 NNYSD-----SWMTLFRWQHVVHTF--MLPFLRLSMLLSQSIIFV-----SQ 278
DB 238 LEMFSDVPDEELTRMSRWFVNLQTFYFPIILSFARLSWCLQSILFVLPNGOAHKPSGAR 297
QY 279 MPTHYDYRYNTAIYEOVGLSLHWASLGQLY-FLPDWSTRIMEFLVSLHVGFLSHVY 337
DB 298 VP-----ISLVEQLSLAMHTWYLATMFLFIKDPVNMVLYFLVSQAACGNLLAIVF 348
QY 338 TPNHYSVEKFAALSSNIMSYACLIQIMTRNMRPGRFIDWLWGLNLYQIEHHLFPTMPRHN 397
DB 349 SLNHGMPVISKEEAVIDMDEFTKQIITGRDVHFGLFANWFTGGLNLYQIEHHLFPTMPRHN 408
QY 398 LNTVMPLVKEFAAANGPLVMVDYFTGFWLEIEQFNRNIANVAALTK 444
DB 409 FSKIQPAVETLCKKYNVRYHTTGMIETGAEVFSRLNEVSKAASKMGK 455
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## RESULT 9

```
US-09-227-613-41
; Sequence 41, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradiip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: xaa at position 458 is unknown or other.
US-09-227-613-41
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Query Match 25.8%; Score 629; DB 4; Length 458;  
Best Local Similarity 33.0%; Pred. No. 1.1e-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

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QY 4 REOEHEPFIKIDGKCQIDDAVLRSHPGGSAITTYKNMDATVFTHTGSKAEAYQWLT 63
DB 25 KKDAEAPFLMIIDNKVYDREFV-PDHPGGSVILTHVGKDGTDVDFTEH---PEA-AWET 79
QY 64 ELKKECTQEPIDPKDPIKIGDIDVNMGTFNISEKRSQAQINKSFTDLRMVRRAEGLMD 123
DB 80 LANFVYGDIDESDRDIKNDFF-----AAEVRK-----LRTLFSQSLGYD 118
QY 124 GSPFLFYIRKI-----LETITLILFAFYLOYHTY-YLPSSAILMGVAAQGLWLIHEFAHQ 177
DB 119 SSKAYYAFKVSFNLCTWGLSTVIVAKWGQTSTLANVLSAALLGLFWQCCGWLADHFLHQ 178
QY 178 LFKNRYNDLASFYVGNFLQGSFGGKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237
DB 179 VFQDRFWGDLFGAFLGGVCGQFSFSSWKKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237
QY 238 NNYSD-----SWMTLFRWQHVVHTF--MLPFLRLSMLLSQSIIFV-----SQ 278
DB 238 LEMFSDVPDEELTRMSRWFVNLQTFYFPIILSFARLSWCLQSILFVLPNGOAHKPSGAR 297
```





SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-834-033A-6

Query Match 22.8%; Score 555; DB 3; Length 355;  
Best Local Similarity 34.5%; Pred. No. 2e-47;  
Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;  
QY 112 LRMVRAGLMDGSPFLFYRKI-----LETITILFAFYLOYHTY-YLPSSAILMGVAQQ 165  
DB 5 LRTFQSLGYDSSKAYAFKVSFNLGICWGLSTVIVAKWGOTSTLANVLSAALLGLFWQQ 64  
QY 166 LGWLIHFAHQLFKNRYNDLASFYVGNFQSGGKQHNHHAAATNVVGRDGLD 225  
DB 65 CGWLADFLHHQVQDRFWGDLFGAFLGGVCGGFSWKKDKHNTTHAAAPNVHGEDPDID 124  
QY 226 LVPFYATVAEHLNYSQD-----SWVMTLFRQHVHTF--MLPFLRLSLQSLIFV- 276  
DB 125 THPL-LTWSEHALEMFSDVPDEELTRMSRFVNLQTFYFPILSFARLSWCLQSLIFVL 183  
QY 277 -----SOMPTHYDYRNTAIYEQVGLSLHAWSLGOLY-FLPDWSTRIMFVLVS 325  
DB 184 PNGAHPKSGARVP-----ISLVEQLSLAHHTWTLATMFLFIKDPVNNMLVFLVS 234  
QY 326 HLVGFLLSHVVTNHYSVKFASSNIMSNYACLIQMTTRNMRPGRFIDWLWGGLNYOI 385  
DB 235 QAVCGNLLAIVFSLNHNMGVPSKEEAVDMDEFTKQIITGRDVHGLFANFTGGLNYOI 294  
QY 386 EHLFPMPRLNLTVMPLVKEFAAANGLPYVDDYFTGFWLEIEQFRNIANVAKLTK 444  
DB 295 EHLFPSPMRHNSKIOPAVETLCKKNVRYHTTGMEGTAEVFSRLNEVSKAASKMGK 353

## RESULT 14

US-09-363-574-5  
Sequence 5, Application US/09363574  
Patent No. 6136574  
GENERAL INFORMATION:  
APPLICANT: KNUZON, DEBORAH  
APPLICANT: MURKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THURMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363.574  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-202 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716

TELEX: N/A  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-363-574-5

Query Match 22.8%; Score 555; DB 4; Length 355;  
Best Local Similarity 34.5%; Pred. No. 2e-47;  
Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;  
QY 112 LRMVRAGLMDGSPFLFYRKI-----LETITILFAFYLOYHTY-YLPSSAILMGVAQQ 165  
DB 5 LRTFQSLGYDSSKAYAFKVSFNLGICWGLSTVIVAKWGOTSTLANVLSAALLGLFWQQ 64  
QY 166 LGWLIHFAHQLFKNRYNDLASFYVGNFQSGGKQHNHHAAATNVVGRDGLD 225  
DB 65 CGWLADFLHHQVQDRFWGDLFGAFLGGVCGGFSWKKDKHNTTHAAAPNVHGEDPDID 124  
QY 226 LVPFYATVAEHLNYSQD-----SWVMTLFRQHVHTF--MLPFLRLSLQSLIFV- 276  
DB 125 THPL-LTWSEHALEMFSDVPDEELTRMSRFVNLQTFYFPILSFARLSWCLQSLIFVL 183  
QY 277 -----SOMPTHYDYRNTAIYEQVGLSLHAWSLGOLY-FLPDWSTRIMFVLVS 325  
DB 184 PNGAHPKSGARVP-----ISLVEQLSLAHHTWTLATMFLFIKDPVNNMLVFLVS 234  
QY 326 HLVGFLLSHVVTNHYSVKFASSNIMSNYACLIQMTTRNMRPGRFIDWLWGGLNYOI 385  
DB 235 QAVCGNLLAIVFSLNHNMGVPSKEEAVDMDEFTKQIITGRDVHGLFANFTGGLNYOI 294  
QY 386 EHLFPMPRLNLTVMPLVKEFAAANGLPYVDDYFTGFWLEIEQFRNIANVAKLTK 444  
DB 295 EHLFPSPMRHNSKIOPAVETLCKKNVRYHTTGMEGTAEVFSRLNEVSKAASKMGK 353

## RESULT 15

US-09-363-526-5  
Sequence 5, Application US/09363526  
Patent No. 6410288  
GENERAL INFORMATION:  
APPLICANT: KNUZON, DEBORAH  
APPLICANT: MURKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THURMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363.526  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-201 USA  
TELECOMMUNICATION INFORMATION:

Search completed: July 2, 2003, 19:28:43  
Job time : 18.4603 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 12:59:11 ; Search time 3361.32 Seconds  
(without alignments)  
11039.134 Million cell updates/sec

Title: US-09-857-583-3  
Perfect score: 1275  
Sequence: 1 atttttttcgaatgaagt.....gcggggaagctctataagg 1275

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- GenEmbl:\*
- 1: gb\_ba.\*
  - 2: gb\_htg.\*
  - 3: gb\_in.\*
  - 4: gb\_om.\*
  - 5: gb\_ov.\*
  - 6: gb\_pat.\*
  - 7: gb\_ph.\*
  - 8: gb\_pl.\*
  - 9: gb\_pr.\*
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  - 11: gb\_sts.\*
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  - 34: em\_htg\_pln.\*
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  - 36: em\_htg\_mam.\*
  - 37: em\_htg\_vrt.\*
  - 38: em\_sy.\*
  - 39: em\_htgo\_hum.\*
  - 40: em\_htgo\_mus.\*
  - 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	121.6	9.5	1374	8	AF306634	AF306634 Mortierel
3	121.6	9.5	1617	6	AR080598	AR080598 Sequence
4	121.6	9.5	1617	6	AR098439	AR098439 Sequence
5	121.6	9.5	1617	6	AR136018	AR136018 Sequence
6	121.6	9.5	1617	8	AF110510	AF110510 Mortierel
7	118.4	9.3	1374	8	AF307940	AF307940 Mortierel
8	118.4	9.3	1374	8	AF465281	AF465281 Mortierel
9	118.4	9.3	1374	8	AF465282	AF465282 Mortierel
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14	108.8	8.5	1344	3	AF078796	AF078796 Caenorhab
15	108.8	8.5	1344	6	AX020906	AX020906 Sequence
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17	107.4	8.4	1380	8	AX467717	AX467717 Sequence
18	107.4	8.4	1380	8	AF419296	AF419296 Pythium i
19	103.2	8.1	1071	8	AF307941	AF307941 Mortierel
20	103.2	8.1	1644	8	AF307942	AF307942 Mortierel
21	79.4	6.2	1546	8	AB052086	AB052086 Mucor cir
22	71.6	5.6	1467	6	AX058832	AX058832 Sequence
23	71.6	5.6	2040	6	AX058830	AX058830 Sequence
24	71.6	5.6	2040	8	CPU250734	CPU250734 Ceratodon
25	71.2	5.6	96312	2	AP005554	AP005554 Oryza sat
26	70	5.5	44274	1	SCHG3	AL442629 Streptomy
27	69.8	5.5	1594	6	AX007239	AX007239 Sequence
28	69.8	5.5	1610	8	BNJ4160	AJ224160 Brassica
29	69.6	5.5	1788	8	AF031194	AF031194 Triticum
30	68.6	5.4	1434	6	AX481613	AX481613 Sequence
31	68.6	5.4	1434	6	AX481942	AX481942 Sequence
32	68.6	5.4	1669	8	AY082393	AY082393 Phaeodact
33	60.8	4.8	1591	8	HACYTB5RN	X87143 Helianthus
34	60.8	4.8	1606	6	AX007273	AX007273 Sequence
35	58.6	4.6	2335	8	AB085689	AB085689 Saccharom
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38	56	4.4	1652	8	AY087345	AY087345 Arabidops
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ALIGNMENTS

RESULT 1  
AF139720  
LOCUS AF139720 1275 bp mRNA linear PLN 29-JUL-1999  
DEFINITION Euglena gracilis delta8 fatty acid desaturase (efd1) mRNA, complete cds.  
ACCESSION AF139720  
VERSION AF139720.1 GI:5639723  
KEYWORDS  
SOURCE Euglena gracilis.  
ORGANISM Euglena gracilis  
Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.  
REFERENCE 1 (bases 1 to 1275)  
AUTHORS Wallis J.G. and Browse J.  
TITLE The Delta8-desaturase of Euglena gracilis: an alternate pathway for synthesis of 20-carbon polyunsaturated fatty acids





University, 94 Weijin Road, Tianjin 300071, People's Republic of China

FEATURES  
source  
CDS

Location/Qualifiers  
1..1374  
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/db\_xref="GI:11559824"  
/translation="MAAPSVRTFTRAILNBAELNEKKDAEPLMIIDNKVYDVR  
EVPDPGGSVLTHVGDGTDVDFHPEAAWETLANFYVGDIDESRAIKNDFFAA  
EVRKLRTFSLGYDYSSKAYAEKFNLCITWGLSTIVAKWQSTLNIYLSAALL  
GLFWQCQDLHDFLHQVDFQDFWGLFGLGCVGFSWMMKDKHRAHPNV  
HGEPDIDTHPLTWSEHALEFSDVDELTWMSREWLNQWYFPILSFARLW  
CLOSILVLPNGQHPKSARVSIISLEQLSLAMHTWYLATMELFIKDPVNMVYEL  
VSOAVCGNLLAIYFSLNHNMPVISKEAVDMDFTKIITGRDVPGLFANWFTGGL  
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BASE COUNT 260 a 393 c 359 g 362 t

Query Match 9.5%; Score 121.6; DB 8; Length 1374;  
Best Local Similarity 49.3%; Pred. No. 2.5e-22;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

QY 394 GGCAGTGTTCCTGGGATGCACATCAACAGATGGCTGGCTTTCTCATGACATTTGCCA 453  
DB 468 GGCTCGCTCTTGGTCTCTTCTGGCAGCAGTGTGGATGGTGGCGCAGACTTTTGCA 527

QY 454 CCACAGACTTTCAAGAGCGGACTGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513  
DB 528 CCACAGCTCTCCAGGACCGTTCTGGGTGATCTTTTCGGCGCTCTTGGGAGGTGT 587

QY 514 TCTGCAAGTTTTTCCTGGATCATGTTGGAAGCAGACACATGACATCATTCGCGCAAC 573  
DB 588 CTGCAGGCGTTCTCGCTCATGTGTGGAAGGACAGCACAACACTCACACGCGCGCCC 647

QY 574 CAATGTTCAAGGGCAGCCCTGATTTGACAACTCCCGCTTAGCCTGCTGAGGA 633  
DB 648 CAACGTCCAGGAGATCCGACATGACACTCACCTCTGTTGACGTGGAGTGAGCA 707

QY 634 -----TGACCTCACGCGGCGTCCACCGATTTCGCGCAA 666  
DB 708 TGCTTGAGATGTTCTCGGACGCTCCCTGACGAGGAGCTGACCCGCAATGCTGCGCTT 767

QY 667 GCTCATTCAGTTCAGCAGTACTATTTCTTGTCATCTGATCTTGTTCGGTTCATTTG 726  
DB 768 CATGTCCTTAACACAGACTGGTGTACTTTCCCATTTCTCTGTTGCCCGCTCTCTCGT 827

QY 727 GTGTTTCAGTGCCTGTTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780  
DB 828 GTGCTTCAGTCCATCTCTTCTTGCTGCTAACGGTACGGCCACAAAGCCCTCTGGAC 887

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DB 888 CGGTGTGTCATTCTTGGTTCGAGCAGCTGCTCTTGCCATGCACTGGACCTGGTACCT 947

QY 841 CCTGTTCCACTTATTTCTTATGCCAGCATCTCATACGCTGTTGGTGTGTTTTCCTTTC 900  
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QY 1021 CATGACATTCGCGAGGAGATATATCAGACATTTGGTTTTTCGGAGGCTTGAATACCAGAT 1080  
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QY 1081 TGAGCACCATTGTTGGCGCACCTCCTCGCCACACACCTGACAGCGGTTAGCTACCAAGT 1140  
DB 1188 TGAGCACCATTGTTGGCTTCCTCGATGCTCGCCACAACATTTTCAAGATCCAGCTGCTGT 1247

QY 1141 GGAACAGCTGTCCAGAGACACAACTGCCGTATCGGAACCC 1182  
DB 1248 CGAGACCTTGTGCAAAAAGTATGGTGTCCGATACCACACCAC 1289

RESULT 3  
LOCUS AR080598  
DEFINITION Sequence 1 from patent US 5968809.  
ACCESSION AR080598  
VERSION AR080598.1 GI:10007328  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1617)  
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.-S., Thurmond,J. and Chaudhary,S.  
TITLE Methods and compositions for synthesis of long chain  
poly-unsaturated fatty acids  
JOURNAL Patent: US 5968809-A 1 19-OCT-1999;  
FEATURES Location/Qualifiers  
Source 1..1617  
BASE COUNT 310 a 470 c 410 g 427 t  
ORIGIN

Query Match 9.5%; Score 121.6; DB 6; Length 1617;  
Best Local Similarity 49.3%; Pred. No. 2.5e-22;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

QY 394 GGCAGTGTTCCTGGGATGCACATCAACAGATGGCTGGCTTTCTCATGACATTTGCCA 453  
DB 538 GGCTCGCTTTTGGTCTCTTCTGGCAGCAGTGGTGGCTGCGACATTTTGTGCA 597

QY 454 CCACAGACTTTCAAGAACCGGACCTGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513  
DB 598 TCACAGGTCTTCCAGGACCGTTCCTGGGGTGATCTTTTCGGCGCTCTTTCGGAGGTGT 657

QY 514 TCTGCAAGTTTTTCCTGACATGTTGGAAGGACAGACAACTGACATCATTCGCGCAAC 573  
DB 658 CTGCCAGGCTTCTCTGCTCTGTTGGTGGAGGACAGACAACTCACACGCGCGCCC 717

QY 574 CAATGTTCAAGGGCAGCACCCTGATATTGACAACTCCCGCCCTTAGCCTGGTCTGAGGA 633  
DB 718 CAACGTCCAGCGGAGGATCCCGACATGACACCCACCTCTCTGACCTGGAGTGAGCA 777

QY 634 T-----GAGTGCACAGCGGCGTCCACCGATTTCGCCCAA 666  
DB 778 TGCGTTGGAGATGTTCTCGATGTTCCAGATGAGGAGCTGACCCGCAATGTTGGCGCTT 837

QY 667 GCTCATTCAGTTCACAGCAGTACTATTTCTTGGTCACTCTGATCTTGTTCGGCTTCATTTG 726  
DB 838 CATGGTCTCGAACACAGACCTGGTTTACTTCCCATTTCTCTGTTGCCCGCTCTCTCCTG 897

QY 727 GTGTTTCCAGTGGTGTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780  
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QY 781 CTATCGCTCTCAGTATAAGAGAGGCCATTTGGCTCGCCCTGCACCTGGACCTTGAAGGC 840  
DB 958 GGGTGTGCCCATCTCGTGTGCGAGCAGCTGTGCTTGGATGACATGACCTGGACCTGGTACCT 1017

QY 841 CCTGTTCCACTTATTTCTTTATGCCAGCATCTTCACATCGCTCTGTTGGTGTGTTTTCGTTTC 900  
DB 1018 CGCCACCATTGTTCTCTTATCAAGGATCCCGTCAACATGCTGGTGTACTTTTGGGTGTC 1077



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Db 778 TCGGTTGGAGATGTTCTCGGATGCCAGATGAGGAGTGCACCCGCGATGTGTCGCGTTT 837
Qy 667 GGTCAATTCAGTTCCAGCAGTACTATTTCTTGTGTCATCTGTATCTTGTTCGCGTTCATTG 726
Db 838 CATGTCCTGACACAGACCTGTTTACTTCCCATCTCTCGTTGCGCGTCTCTCTG 897
Qy 727 GTGTTTCAGTCGCGTGTACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780
Db 898 GTGCTCCAGTCCATCTCTTTGTGCTGCCTAACGGTCAAGGCGCCACAGCCCTCGGGCG 957
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RESULT 6  
AF110510  
LOCUS Mortierella alpina delta-6 fatty acid desaturase mRNA, complete cds.  
DEFINITION AF110510.1 GI:6448795  
VERSION AF110510  
KEYWORDS  
SOURCE  
ORGANISM Mortierella alpina.  
Mortierella alpina  
Eukaryote; Fungi; Zygomycota; Zygomycetes; Mucorales;

REFERENCE 1 (bases 1 to 1617)  
Huang, Y.S., Chaudhary, S., Thurmond, J.M., Bobik, E.G. Jr., Yuan, L., Chan, G.M., Kirchner, S.J., Mukerji, P. and Knutzen, D.S.  
Cloning of delta12- and delta6-desaturases from Mortierella alpina and recombinant production of gamma-linolenic acid in Saccharomyces cerevisiae  
Lipids 34 (7), 649-659 (1999)  
MEDLINE 99406036  
PubMed 10478922

REFERENCE 2 (bases 1 to 1617)  
Knutzen, D.S.  
Direct Submission  
TITLE Submitted (02-DEC-1998) Calgene LLC, 1920 Fifth St., Davis, CA 95616, USA  
JOURNAL Location/Qualifiers

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## RESULT 10

AF465283

LOCUS

DEFINITION Mortierella alpina delta 6 fatty acid desaturase (GLD6D-1) gene, complete cds.

ACCESSION

AF465283

VERSION

AF465283.1

KEYWORDS

SOURCE

ORGANISM

Mortierella alpina.

Mortierella alpina.

Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;

Mortierellaceae; Mortierella.

1 (bases 1 to 1947)

Liu, L., Li, M., Hu, G. and Xing, L.

Cloning and sequence analysis of the delta 6 fatty acid desaturase

gene from Mortierella alpina ATCC16266 genomic and cDNA

Unpublished

2 (bases 1 to 1947)

Xing, L., Liu, L., Li, M. and Hu, G.

Direct Submission

Submitted (04-JAN-2002) Microbiology, Naikai University, Weijiang

road 94th, Tianjin 300071, China

Location/Qualifiers

1. 1947

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ACCESSION AB020032
VERSION AB020032.1 GI:6070339
KEYWORDS delta-6 fatty acid desaturase.
SOURCE Mortierella alpina (strain:1S-4) cDNA to mRNA.
ORGANISM Mortierella alpina
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
Mortierellaceae; Mortierella.
1 (sites)
REFERENCE Sakuradani, E., Kobayashi, M. and Shimizu, S.
AUTHORS Delta6-fatty acid desaturase from an arachidonic acid-producing
TITLE Mortierella fungus. Gene cloning and its heterologous expression in
a fungus, Aspergillus
JOURNAL Gene 238 (2), 445-453 (1999)
MEDLINE 20035749
AUTHORS 2 (bases 1 to 1590)
TITLE Kobayashi, M., Sakuradani, E. and Shimizu, S.
JOURNAL Direct Submission
SUBMITTED (16-NOV-1998) Michihiro Kobayashi, Graduate School of
Agriculture, Kyoto University, Division of Applied Life Sciences;
Kitashirakawa, Oiwake-cho, Sakyo-ku, Kyoto, 606-8502, Japan
(Tel:81-75-753-6114)
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VERSION AF031477.1 GI:3088519
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SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
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AUTHORS Rhabditidae; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
Savanna, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G.,
Christie, W.W., Shewry, P.R. and Napier, J.A.
Expression of a borage desaturase cDNA containing an N-terminal
cytochrome b5 domain results in the accumulation of high levels of
delta6-desaturated fatty acids in transgenic tobacco
proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
97268723
JOURNAL 9108131
MEDLINE 2 (bases 1 to 1463)
REFERENCE Napier, J.A., Hey, S.J., Lacey, D.J. and Shewry, P.R.
AUTHORS Identification of a Caenorhabditis elegans
TITLE Delta6-fatty-acid-desaturase by heterologous expression in
Saccharomyces cerevisiae
JOURNAL Biochem. J. 330 (Pt 2), 611-614 (1998)
MEDLINE 98149727

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PUBMED 9480865
REFERENCE 3 (bases 1 to 1463)
AUTHORS Napier, J. A.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1997) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK
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RESULT 13
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LOCUS AX003603 1463 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 1 from Patent WO9927111.
ACCESSION AX003603
VERSION AX003603.1 GI:9927413
KEYWORDS Caenorhabditis elegans.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 1463)
AUTHORS Napier, J. A.
TITLE Desaturase genes and their use
JOURNAL Patent: WO 9927111-A 1 03-JUN-1999;
UNIV BRISTOL (GB); NAPIER JOHNATHAN A (GB)
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## RESULT 14

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LOCUS AF078796 1344 bp mRNA linear INV 11-DEC-1998
DEFINITION Caenorhabditis elegans delta 5 fatty acid desaturase (des-5) mRNA,
complete cds.
ACCESSION AF078796
VERSION AF078796.1 GI:4003522
KEYWORDS
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 1344)
Michaelson, L.V., Napier, J.A., Lewis, M., Griffiths, G., Lazarus, C.M.
and Stobart, A.K.
Functional identification of a fatty acid delta5 desaturase gene
from Caenorhabditis elegans
FEBS Lett. 439 (3), 215-218 (1998)
JOURNAL 99059458
MEDLINE
PUBMED 9845325
REFERENCE 2 (bases 1 to 1344)
AUTHORS Michaelson, L.V., Napier, J.A., Lazarus, C.M., Griffiths, G. and
Stobart, A.K.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1998) Biological Sciences, University of Bristol,
Woodland Road, Bristol BS8 1UG, UK
LOCATION/Qualifiers
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Best Local Similarity 49.0%; Pred. No. 8.7e-19;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 19:20:22 ; Search time 31.3774 Seconds  
(without alignments)  
1638.178 Million cell updates/sec

Title: US-09-857-583-2  
Perfect score: 2435  
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Scoring table: BLOSUM62  
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Searched: 440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	533.5	21.9	459	9	US-09-967-477B-8
5	408.5	16.8	432	9	US-10-191-513A-9
6	408.5	16.8	465	9	US-10-191-513A-38
7	403.5	16.6	448	12	US-10-029-756-5
8	402.5	16.5	444	9	US-10-191-513A-12
9	396.5	16.3	444	9	US-10-262-617-3
10	396	16.3	444	9	US-10-191-513A-42
11	387	15.9	452	12	US-10-029-756-27
12	372.5	15.3	445	9	US-10-262-617-1
13	347	14.3	365	9	US-10-156-761-9835
14	312.5	12.8	286	9	US-10-102-806-650
15	311	12.8	356	9	US-10-191-513A-18
16	298.5	12.3	287	9	US-10-191-513A-14
17	298.5	12.3	288	9	US-10-191-513A-15
18	281.5	11.6	353	9	US-10-156-761-9130
19	277	11.4	439	9	US-09-967-477B-4

20	250.5	10.3	360	9	US-10-191-513A-39	Sequence 39, Appl
21	248.5	10.2	519	9	US-09-967-477B-2	Sequence 2, Appl
22	247.5	10.2	515	9	US-09-849-199A-19	Sequence 19, Appl
23	244.5	10.0	515	9	US-09-849-199A-18	Sequence 18, Appl
24	244.5	10.0	515	9	US-09-849-199A-20	Sequence 20, Appl
25	239.5	9.8	515	9	US-09-849-199A-21	Sequence 21, Appl
26	230.5	9.5	446	10	US-09-903-456-30	Sequence 30, Appl
27	230.5	9.5	447	9	US-10-191-513A-10	Sequence 10, Appl
28	230	9.4	347	9	US-10-191-513A-40	Sequence 40, Appl
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31	200.5	8.2	315	9	US-10-191-513A-16	Sequence 16, Appl
32	184	7.6	370	10	US-09-815-242-5200	Sequence 5200, Ap
33	178	7.3	335	9	US-09-849-199A-26	Sequence 26, Appl
34	165.5	6.8	387	9	US-09-981-124-13	Sequence 13, Appl
35	165.5	6.8	387	9	US-10-224-446-5	Sequence 5, Appl
36	165.5	6.8	387	10	US-09-837-751-33	Sequence 33, Appl
37	163	6.7	219	9	US-10-191-513A-19	Sequence 19, Appl
38	161	6.6	309	10	US-09-885-188-8	Sequence 8, Appl
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41	147.5	6.1	384	10	US-09-995-297-6	Sequence 6, Appl
42	147.5	6.1	384	10	US-09-995-297-18	Sequence 18, Appl
43	146.5	6.0	384	10	US-09-995-297-10	Sequence 10, Appl
44	145.5	6.0	384	10	US-09-995-297-14	Sequence 14, Appl
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ALIGNMENTS

RESULT 1

US-10-191-513A-11  
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; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; NAME/KEY: VARIANT  
; LOCATION: (458)...(458)  
; OTHER INFORMATION: Xaa = Unknown or other at position 458  
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Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

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; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Paridip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; PRIOR FILING DATE: 2002-09-25  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR FILING DATE: 1997-04-11  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (458)....(458)  
; OTHER INFORMATION: Xaa = Unknown or other at position 458  
US-10-191-513A-41

Query Match 25.8%; Score 629; DB 9; Length 458;  
Best Local Similarity 33.0%; Pred. No. 5.9e-51;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;  
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Db 238 LEMFSDVPDELTMRWSRFVNLQTFYFPLSPARLSWCLOSLFLVLPNGQAHKPSGAR 297  
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## RESULT 3

US-10-191-513A-17  
; Sequence 17, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Paridip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (323)....(323)  
; OTHER INFORMATION: Xaa = Unknown or other at position 323  
US-10-191-513A-17

Query Match 22.2%; Score 541; DB 9; Length 323;  
Best Local Similarity 36.5%; Pred. No. 7.3e-43;  
Matches 113; Conservative 55; Mismatches 112; Indels 30; Gaps 6;  
QY 155 SAILMGVAMQOLGWLIEFAHQLHPKRNRYNDLASFYVGNFLQGFSSGKWEQHNHHA 214  
Db 21 SAALLGLFWQCGWLAHDFLHHQVFDQDRFGDGLFGAFLGGVCGQGFSSSWKDKHNTTHA 80  
QY 215 TNYVGRDGLDLVPFYATVAEHLNYSQD-----SWMTLFRQHVHTF--MLPFLRL 266  
Db 81 PNHVGEDPDIDTHPL-LTWSEHALEMFSVPDELTMRWSRFVNLQTFYFPLSPARL 139  
QY 267 SWLQSIIFV-----SOMPTHYDYRNTATYEQVGLSLHAWSLGOLY-FLPD 314  
Db 140 SWCLOSLFLVLPNGQAHKPSGARVP-----ISLVEQLSLAHHTWYLATMFLFKD 190  
QY 315 WSTRIMFVLSHLVGGFLSHVHTVFNHYSEKFAKSSNINSNYACLOIMTTRNNRPGRI 374

Db 191 PVMNLVFLVSAQVGNLLAIVFSLNHNHMPVSKEEAVDMDEFTTKIITGRDVBHPLFA 250  
Qy 375 DMLWGLNLYQIEHHLPPTMPRNLNTVMPVLEFEFAAANGLPYVDDYFTGFWLEIEQFRN 434  
Db 251 NMFTGGLNLYQIEHHLPSPRHRNFSKIOPAVETLCKKYNVRYHTTGMIETAEVFSRLNE 310  
Qy 435 IANVAKLTK 444  
Db 311 VSKAASKNGK 320

RESULT 4  
US-09-967-477B-8  
; Sequence 8, Application US/09967477B  
; Patent No. US20020156254A1  
; GENERAL INFORMATION:  
; APPLICANT: Xiao Qiu  
; APPLICANT: Haiping Hong  
; TITLE OF INVENTION: FAD4, FADS-2, AND FAD6, NOVEL  
; FILE REFERENCE: BNZ-001  
; CURRENT APPLICATION NUMBER: US/09/967,477B  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/236,303  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/297,562  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Thraustochytrium sp.

US-09-967-477B-8

Query Match 21.9%; Score 533.5; DB 9; Length 459;  
Best Local Similarity 31.6%; Pred. No. 6e-42;  
Matches 137; Conservative 70; Mismatches 186; Indels 41; Gaps 12;

Qy 29 SHPGSATYTKNDATTVFHTFGSKRAYQWLTKKECTQPEIPDKDDPIKIGD 88  
Db 42 SHPGSVMLTQAGEDAFVAFHPSSALK---LLEQFYVGDVDETSKAEIEGPAS--- 95

Qy 89 DYNMGTENISERSAQINK--SFTDLRMVRAEGLMDGSPLEYIRKILET----IFTIL 141  
Db 96 -----DEERARRERINEFIASRYRLRVKVGMDGLYDASALYAKLVSTFGIAVLSMA 148

Qy 142 FAFYLYQYHTYLPSSAILMGVAAQQLGLIHEFAHQLFKNRYNDLASFYVGNFLOGESS 201  
Db 149 ICFFNSFAMYVAGVINGLFLYQQSGWLHDFLNQVCENRTLGNLGLVGNAGQFSV 208

Qy 202 GQWKEQHNHVAATNY-----VGRDGLDLVPFYATVAEHLNNYSQDSWYMTLFRMQ 253  
Db 209 QWKNKHLHVAVNLHSAKDEGFIG-DPDIOTMPLLAWSKEMARKAFESAHPPIRQ 267

Qy 254 VHVTFMPLFLRLSLQSIIFV-SOMPHYDYNTNTAIYEQVLSLHWASLGOLYEL 312  
Db 268 AFLYFPLLLARLSLAQSFYVTFEFSFGIEDKVEFDG-PEKAGLIVHVIWQALPYFC 326

Qy 313 -PDWSTRIMFFLVSHLVGGFLSHVYTFNHYSEKFEALSSNTMSNVACIQIMTRMRPG 371  
Db 327 NMSLEGVAYFLMGQASCLLALVFSIGHNGMSVYERETK--PDFWQLQVTTTRNIRAS 384

Qy 372 RFIDLWGLNLYQIEHHLPPTMPRNLNTVMPVLEFEFAAANGLPYVDDYFTGFWLEIEQ 431  
Db 385 VEMDNFTGGLNYQIDHHPPLVPRNLNPKVNVLIKSLCKEFDIPF-----HEYGFW---EG 437

Qy 432 FRNIANVAKLTK 445  
Db 438 IYEVVDHLADISKE 451

RESULT 5

US-10-191-513A-9  
; Sequence 9, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardiip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295. US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 432  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (432)...(432)  
; OTHER INFORMATION: Xaa = Unknown or other at position 432

US-10-191-513A-9

Query Match 16.8%; Score 408.5; DB 9; Length 432;  
Best Local Similarity 27.7%; Pred. No. 3.4e-30;  
Matches 119; Conservative 64; Mismatches 167; Indels 79; Gaps 13;

Qy 18 KWCQIDDAV-----LRSHPGGS-AITTYKNMDATTVFHTFGTSKEAYOWLT-----EL 65  
Db 22 RMLVIDRKYNISEFTRRHRPGGSRVISHYAGQATDPFVAFHINKGLVKYKMNLSLIGEL 81

Qy 66 KKECTQPEIPDKDDPIKIGDIDVNMGTENISERSAQINKSFTDLRMVRAEGLMDGS 125  
Db 82 SPQSPSEF-----TKNKELTDEPRELRATVERMGLMKAN 116

Qy 126 PLEYIRKILETIFTILFAFYLO---YHTYLP---SAILMGVAAQQLGLIHEFAHHOLF 179  
Db 117 HVFFELYLLH-ILLDGAAWLTWVFGTSELPFLLCALLSAVOAQAQGLQHDYGLSVY 175

Qy 180 KNRYYNDLASFYVGNFLOGESSGQWKEQHNHVAATNVVGRDGLDLVPFYATVAEHLNN 239  
Db 176 RPKWNHLVHKFVIGHLKGASANNHHRHQHAKPNIFHKDPPVNMHLVFLGEWQPIE 235

Qy 240 YSODSWMTLFRWQHVVHTFMPLFLRLSLQSIIFVSOMPHYDYNTNTAIYEQVGLS 299  
Db 236 YGCKKLKLYPNHQHEVFFLIGPPLLPYFQYQIIM-----TMIVHKNWVD 282

Qy 300 LHWANSLGOLYFLPDMSTRIMFFLVSHLVGG-----FLLSH-----VVTFNHYSEK 347  
Db 283 LAWAVS-----YYIRFFTYIPFY---GILGALLFLNFRFLESHFWFVMTOMNHVME-- 333

Qy 348 ALLSNTMSNVACIQIMTRMRPGRFDLWGLNLYQIEHHLPPTMPRNLNTVMPVLE 407  
Db 334 -IDQEAYRDFSSQLTATCNVEOSFFNDWFSGLHNFQIEHHLPPTMPRNLNHTAPLVKS 392

Qy 408 FAAANGLPY 416  
Db 393 LCAKHGIEY 401

RESULT 6

US-10-191-513A-38  
; Sequence 38, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:

APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pardip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Tapas, Das  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295, US, D3  
CURRENT APPLICATION NUMBER: US/10/191,513A  
CURRENT FILING DATE: 2002-09-25  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 465  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (432)...(432)  
OTHER INFORMATION: Xaa = Unknown or other at position 432  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (458)...(458)  
OTHER INFORMATION: Xaa = Unknown or other at position 458  
US-10-191-513A-38

Query Match 16.8%; Score 408.5; DB 9; Length 465;  
Best Local Similarity 27.7%; Pred. No. 3.8e-30;  
Matches 119; Conservative 64; Mismatches 167; Indels 79; Gaps 13;  
QY 18 KWCIDDAV-----LRSHPGGS-AITTKNMDATTVFHTGSKSEAYQWL-EL 65  
DB 22 RMLVIDRVKYNISEFRRHPGGSVISHYAGQATDPFVAFHINKGLVKYKMSLLIGEL 81  
QY 66 KKECTQPEIPDKDDPIKIGDDVNMGTNISEKSAQINKSFDTLRMRVRAEGLMDGS 125  
DB 82 SPEQSPFEP-----TKNKELTDFEFLRATVERMGLMKAN 116  
QY 126 PLFYIRKILETIFTLFAVLO---YHTYLP---SAILMGVAQQLGWLHIEFAHQHOLF 179  
DB 117 HVFFLLYLH-ILLDGAWLTLWVFGTSELPFLLCVLLLSAVQAQAGWLQHDYGHLSVY 175  
QY 180 KRYINDLASFYGNFLQGFSSGGWKEQHNVHHAATNVVGRDGLDLVFPYATVAEHLNN 239  
DB 176 RPKWNHVLHKFVIGHLKGSANWNNRHFQHHAKPNIFHKDPDVMNLHVFLGEMQPIE 235  
QY 240 YSODSNWMLFRQHVHTFPMFLPFLRLSLWLSQIIFVSOMPTHYDYRYNTATYEQVGLS 299  
DB 236 YGKKLKLPLYNHQHEHYFFLIGPLLPYFYQIIM-----TMIVHKNWVD 282  
QY 300 LHWASLGOLYFLPDWSTRMFLVSHLVGG-----FLLSH---VYTFNHYSEKF 347  
DB 283 LAWAVS---YYIRFTIYIPFY---GILGALLFLNFIRESHFWFWVTQMHVNE-- 333  
QY 348 ALSSNMSVACIQIMTTRNMRGRFDLWGLGNTQIEHHLFPTMPRHNLNTVMPLVKE 407  
DB 334 -IDQAYRDWFSQSOLTATCNVESFFDNFSGHLNFQIEHHLFPTMPRHNLKHLAPLVS 392  
QY 408 FFAANGLPY 416  
DB 393 LCAKHGIEY 401

RESULT 7  
US-10-029-756-5  
Sequence 5, Application US/10029756  
Patent No. US20020108147A1  
GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.  
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
DELTA 6-DESATURASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/029,756  
FILING DATE: 21-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,254  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 83832YXWVU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 448 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-029-756-5  
Query Match 16.6%; Score 403.5; DB 12; Length 448;  
Best Local Similarity 27.0%; Pred. No. 1.1e-29;  
Matches 123; Conservative 69; Mismatches 199; Indels 65; Gaps 16;  
QY 12 FIDGKWCQIDDAVLRSHPGGS-AITTKNMDATTVFHTGSKSEAYQWLTELKKECP 70  
DB 24 WISQIGRAYDSQWV-KDHFGSPPLKSLAGQVTDAPVAFHPAS---TW----- 69  
QY 71 TQPEIPDKDDPIKIGDDVNMGTNISEKSAQINKSFDTLRMRVRAEGLMDG----- 124  
DB 70 -----KNLDKFTG-YLKDYSVSEVSKDYRLKLVFEFSKMGLYDKKGHMF 114  
QY 125 SPLFYIRKILE-TIFTLFAFYLYHTYLYLPSAILMGVAQQLGWLHIEFAHQHOLFKNRY 183  
DB 115 ATLCLFAMLFAMSVYGVLFCEGLVHLF---SGCLMGFLWISQGWIGHDAGHVMVSDSR 171  
QY 184 YNDLASFVGNFLQGFSSGGWKEQHNVHHAATNVVGRDGLDLV-----FYATVAEH 236  
DB 172 LNKFMGIFAANCLSGISIGWKNWNNHNAHHAACNLSLEYDPLQYIPFLVSSKFFGSLTSH 231  
QY 237 L--NNYSQDSWMTFLFRQHVHTF--MLPFLRLSLWLSQIIFVSOMPTHYDYRYNTA- 291  
DB 232 FYEKRLTFDS--LSRFFVSQHVHTFYFPCARLNMVYVOSLIMLLTK-----RNVSY 281  
QY 292 -IYEQVGLSLHAWMSLGOLYFLPDWSTRMFLVSHLVGGFLSHVTVTFNHYSEKFPALS 350  
DB 282 RAQELGCLVFSIWIYPLLVSCLPNNGERIMEVIAASLSVTG-MQOVQFSLNHFSSVY-VG 339  
QY 351 SNIMSNTVACIQIMTTRNMRGRFDLWGLGNTQIEHHLFPTMPRHNLNTVMPLVKEFAA 410  
DB 340 KPKGNWFEKQTDGTLDISCPWMDWFGSGQFQIEHHLFPPKPRCNLRKISPYVIELCK 399  
QY 411 ANGLPYWDDYFTGFWLEIEQFRNIANVAKLTKKI 446



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; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa - Unknown or other at position 444
US-10-191-513A-42

Query Match      16.3%; Score 396; DB 9; Length 444;
Best Local Similarity 26.4%; Pred. No. 53e-29;
Matches 123; Conservative 59; Mismatches 168; Indels 116; Gaps 17;

QY 18 KWCIDDAV-----LRSHPGGS-AITTKNMDATTVFTHFGSKSAYQWLT-----EL 65
DB 34 RLVLDKVVYNISEFTRRHGGSKVISHYAGQDATDPVAFHINKGLVKYKMSLLIGEL 93
QY 66 KKECTQEPDIPDKDPIKIDVNMGTNISEKSAQINKSTFD---LRMRVRAGLM 122
DB 94 SPEQSPFEP-----TKNKELTDFELRATVERMGLM 124
QY 123 DGSPLFVIRKILETIFLPAFYLO---YHTYVLP---SAILMGVAQQLGWLHIEFAHH 176
DB 125 KAHVFEFLYLLH-ILLDGAALWLTWVFTSETLPLFLLCAVLLSVAQAQAGWLQHDGHL 183
QY 177 QLFKNRYNDLASFYGNFLQFGSSGCKEQQHNVHHAATNVVGRDGLDLPVYATVAE- 235
DB 184 SVFSTKWNHLLHFVIGLHKGAPASWNNHMQHAKPCNCFKRPDINNHPFFALGKI 243
QY 236 -----HLNNY-----SODSWVWTLFRQHVHTFPLFLSLWLLQSIIF 275
DB 244 LSVELGKQKKKMPYNHQQHYFFLIGPPALLPLYFQW---YIFYFYIQRKKW-----VD 294
QY 276 VSQMPHYDYDYRNTAIYEQVLSLHMAWSLGLYFLPDMSTRIMFLVSHLVGGFFLSH 335
DB 295 LAMWITFYVRF-----LTVPLLLGLKAFGL-----LFIVFLESNWFV-W 335
QY 336 VVTFNHYSVEKFAISNIMSNYACLOIMTTRNMRPGRFIDWLMGGLNYQIEHHLFPMPR 395
DB 336 VTQMNHPMH---IDHRNMDWSTQLLATCNVHKSAFNDWFSGLHNFQIEHHLFPMPR 392
QY 396 HNLNTVMPLVKEFAAANGPLVMDDYFTGF-----WLE 428
DB 393 HNTKRVAPLVOSLCAKRGIEYQSKPLLSAFADIIHSLKESQGLWLD 438

RESULT 11
US-10-029-756-27
; Sequence 27, Application US/10029756
; Patent No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029,756
; FILING DATE: 21-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-029-756-27

Query Match      15.9%; Score 387; DB 12; Length 452;
Best Local Similarity 23.9%; Pred. No. 3.9e-28;
Matches 112; Conservative 81; Mismatches 191; Indels 84; Gaps 17;

QY 4 REQEHEFFFIKIDK-----WCQIDDAVLRSHPGGS-AITTKNMDATTVFTHFGTSK 56
DB 16 RHKSGDLWTSIQKVYDCSRWA-----AEHPGGEVPLSLAGQDVTDFATHPGTA 68
QY 57 -----EAYOWLTCLKKECTQEPDIPDKDPIKIDVNMGTNISEKRSQAINKS 108
DB 69 WRHLDPLFTGYIYLKDF-----EVSEISKDYRLLNE--MSRSGIFEKKGHHIMWT 117
QY 109 FTDLRMRVRAGLMDGSPLFYIRKILETIFLPAFYQYHTYVLPYLSAILMGVAQQLGW 168
DB 118 FVGVAVMMAA-----IVYGLVASESVGVH---MLCGALLGLLWIAAY 157
QY 169 LIHEFAHOLFKNRYNDLASFYGNFLQFGSSGCKEQQHNVHHAATNVVGRDGLDLPV 228
DB 158 VGHDSGHIQVNPTRGYNRITOLIAGNLTGSIWKKWTHNAHHLACHSLDYDPLQHIP 217
QY 229 FYATVAEHLNNYSODSWVMTL-----FRQHVHTF--MLPFLRLSWLLQSIIFV--- 276
DB 218 VFAVSTRLENSITSVFYGRVLKFDVAREFLVSYQHTYVPMVIFGRVNLFIQTFLLLTR 277
QY 277 SQMPHYDYDYRNTAIYEQVLSLHMAWSLGLYFLPDMSTRIMFLVSHLVGGFFLSHV 336
DB 278 RDVDPDALNL-----MGIAVFWTFFPLFVSLCPNMPERFGLVLSFAVTA--IOHV 326
QY 337 -VTFNHYSVEKFAISNIMSNYACLOIMTTRNMRPGRFIDWLMGGLNYQIEHHLFPMPR 395
DB 327 QFTLNHFSGDIY-VGPPKGDWFEKQTKGTIDITCPPWMDWFFGGLQFQLEHHLFPLPR 385
QY 396 HNLNTVMPLVKEFAAANGPLVMDDYFTGFW--LEIQFRNIANYAAK 441
DB 386 GOLRKIAPLARDLCKKHGMPYR---SEGFWDANVRTIRLDAAVQ 429

RESULT 12
US-10-262-617-1
; Sequence 1, Application US/10262617
; Publication No. US20030077747A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
```



; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS  
 ; FILE REFERENCE: PF-0494-1 DIV  
 ; CURRENT APPLICATION NUMBER: US/10/262,617  
 ; CURRENT FILING DATE: 2002-09-30  
 ; PRIOR APPLICATION NUMBER: 09/048,888  
 ; PRIOR FILING DATE: 1998-03-26  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1  
 ; LENGTH: 445  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CD1  
 US-10-262-617-1

Query Match 15.3%; Score 372.5; DB 9; Length 445;

Best Local Similarity 24.7%; Pred. No. 8.8e-27;

Matches 113; Conservative 71; Mismatches 173; Indels 101; Gaps 12;

QY 18 KWCQIDDAV-----LRSHGGGAITYKKN-DATTVFHTHTGSKAYQWLT-----EL 65  
 DB 37 KLVIERVYDISRWQQRHGGSLRIGHGAEDATDAFRAHQDLNFRKFLQPLLIGEL 96  
 QY 66 KKECTQPEIPDKDPKIGIDVNMGTFNISEKRSQAINKSTDLRMVRVRAEGLMDGS 125  
 DB 97 APEPSQ-----DGPL-----NAQLVEDFRALHQAAEDMKLFDA 131  
 QY 126 PLYIRKILETIFLAFYLOQ--HTYILPSAI---LMGVAMQOLGLWIEFAHQHLEK 180  
 DB 132 PTFFAFLGHILAMEVLAWLLIYLLGPGWPSALAAELAISQAQSLQHLQDLGHASIFK 191  
 QY 181 NRYNDLASVFNQFLOGSSGKQHNHHAATNVVGRDGLDLVPFY-----ATV--- 233  
 DB 192 KSWNHVAQRFVGMQLKGFSAHWNFRHQHAKPNIFHKDPDVTVPVFLGSSVEYG 251  
 QY 234 -----AEHLNYSQDSWMTLFRWQHVHTFMPLFRLSWLLOSIFVSMQTHY 283  
 DB 252 KKRRYLPYNQQLHFFLGPPLTLTVNFEENIAYMLVCMQWADLLWAAASYARFTLSY 311  
 QY 284 YDYRNTAIYEQVGLSLHWAWSLGQLYFLPDWSTRIFFLVSHLVGGFLLSHVVTENNYS 343  
 DB 312 LPFYGVGV-----LFFVAVRVLESHFWFIQMHNP 345  
 QY 344 VEKFASSNIMSNACQIMTRMRPGRFIDMLWGLNYQIEHHLFPTMRRHNLNTVMP 403  
 DB 346 KE---IGHEKRDWSSQLAATCNVPSLFTNWFSGHLNFQIEHHLFPRMRRHNSRVAP 402  
 QY 404 LYKEFAAANGLPWVDYFTG-----FWLE 428  
 DB 403 LVKSLCAKGLSYEVKPFPLTALVDIVRSLSKSGDIWLD 440

# RESULT 13

US-10-156-761-9835

; Sequence 9835, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; PRIOR FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 15109  
 ; SEQ ID NO 9835  
 ; LENGTH: 365  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces avermitilis  
 US-10-156-761-9835

Query Match 14.3%; Score 347; DB 9; Length 365;

Best Local Similarity 27.8%; Pred. No. 1.7e-24;

Matches 93; Conservative 62; Mismatches 157; Indels 22; Gaps 7;

QY 108 SFTDLRMVRVRAEGLMDGSPFLFYRKIL--ETIFTILFA--FYLOVHTYLPAILMGVAW 163  
 DB 24 TFAELLKRVKAEGLLDLPRIYIGRLALNTLLLVGFRAFFALGDSWQVLVALNGLCG 83  
 QY 164 QOLGLWIEFAHQHLEKFNRYNDLASVFNQFLOGSSGKQHNHHAATNVVGRDGD 223  
 DB 84 GQSAFMWHDAGHKAMFRSKAASAVGYFHANLVNGVSGMWVYNNHNRHHSNPNHLDMDPD 143  
 QY 224 LDLYPPFYATVAEHLNYSQDSWMTLFRWQHVHTFMPLFRLSWLLOSIFVSMQTHY 283  
 DB 144 IGRRTAIDIKOYPTFRGTQKFIV---RYQSVLFFALLVTEFKMLKTAVLSTAQKGT-- 198  
 QY 284 YDYRNTAIYEQVGLSLHWAWSLGQLYFLPDWSTRIFFLVSHLVGGFLLSHVVTENNYS 343  
 DB 199 -----KRPVLESFLLARAANVLTIVFVLSPLAVAFVLVQQAALGVYFGMIFAPNHHK 253  
 QY 344 VEKFASSNIMSNACQIMTRMRPGRFIDMLWGLNYQIEHHLFPTMRRHNLNTVMP 403  
 DB 254 MEVRDGDDETL-DWLERQVLSRNIRPSLFDIDLYGGLNYQVEHHLFPAMPKPNLARARE 312  
 QY 404 LYKEFAAANGLPWVDYFTGFWLEIEQFRNTAN 437  
 DB 313 LTRAYCAERGVPY-----HEVGFW---ASYREVAS 339

# RESULT 14

US-10-102-806-650

; Sequence 650, Application US/10102806

; Publication No. US20030054421A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA103PIC1

; CURRENT APPLICATION NUMBER: US/10/102,806

; CURRENT FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: 09/925,298

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05881

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 846

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 650

; LENGTH: 286

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-102-806-650

Query Match 12.8%; Score 312.5; DB 9; Length 286;

Best Local Similarity 29.0%; Pred. No. 2.2e-21;

Matches 80; Conservative 46; Mismatches 115; Indels 35; Gaps 6;

QY 153 LPSAILMGVAQQLGWLIEFAHQHLEKFNRYNDLASVFNQFLOGSSGKQHNHVVH 212  
 DB 4 LITAFVLATSOAQAGWLQHDYGLSVYRKRPNWNLHVHFVIGHLKGASANNWNRHFQHH 63  
 QY 213 AATNVVGRDGLDLVPFYATVAEHLNNTSQDSWMTLFRWQHVHTFMPLFRLSWLQS 272  
 DB 64 AKPNIFHKDPVNMHLHVEVLGEWQPIEYCKKKLKLPLYNHQQHEFFLIGPPLIPYFOY 123



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 12:58:36 ; Search time 308.964 Seconds  
(without alignments)  
9293.314 Million cell updates/sec

Title: US-09-857-583-3

Perfect score: 1275

Sequence: 1 atttttttgaatgaagt.....gcggggaaggctctataaag 1275

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1275	100.0	1275	21	AA51233
2	121.6	9.5	1374	21	AA51233
3	121.6	9.5	1374	22	AA51233
4	121.6	9.5	1617	19	AAV63624
5	121.6	9.5	1617	20	AAV63624
6	121.6	9.5	1617	21	AAV63624
7	112.8	8.8	1463	20	AAV63624
8	108.8	8.5	1344	20	AAV63624
9	108.8	8.5	1461	21	AAV63624

10	107.4	8.4	1380	24	AA51233
11	71.6	5.6	1467	22	AA51233
12	71.6	5.6	2040	22	AA51233
13	69.8	5.5	1594	21	AA51233
14	63.4	5.0	1972	21	AA51233
15	61.6	4.8	1934	21	AA51233
16	60.8	4.8	1606	21	AA51233
17	57	4.5	1764	21	AA51233
18	56.4	4.4	2160	22	AA51233
19	56	4.4	657	24	ABQ65917
20	56	4.4	1650	21	AA51233
21	56	4.4	1650	21	AA51233
22	56	4.4	1678	21	AA51233
23	53	4.2	1471	21	AA51233
24	52.6	4.1	2146	22	AA51233
25	52.4	4.1	1465	21	AA51233
26	51.8	4.1	1684	19	AAV34398
27	51.8	4.1	1684	20	AAV34398
28	51.8	4.1	1685	17	AAV30395
29	51.8	4.1	1685	22	AAV30395
30	51.6	4.0	560	22	AAH05343
31	51	4.0	1335	22	AAH19403
32	51	4.0	1474	21	AA51233
33	51	4.0	1575	24	ABL90108
34	51	4.0	1686	19	AAV63641
35	51	4.0	1686	20	AAV63641
36	51	4.0	1686	20	AAV63641
37	51	4.0	1686	21	AAV63641
38	51	4.0	1686	21	AAV63641
39	51	4.0	1686	21	AAV63641
40	51	4.0	1843	19	AAV63642
41	51	4.0	1843	20	AAV63642
42	51	4.0	1843	20	AAV63641
43	51	4.0	1843	21	AAV63641
44	51	4.0	1843	21	AAV63641
45	51	4.0	1843	21	AAV63641

#### ALIGNMENTS

RESULT 1  
AA51233  
ID AA51233 standard; cDNA; 1275 BP.  
XX  
AC AA51233;  
XX  
DT 26-SEP-2000 (first entry)  
XX  
DE E. gracilis' fatty acid delta-8 desaturase coding sequence.  
XX  
KW Fatty acid delta-8 desaturase; polyunsaturated; oil; seed;  
KW infant formula; dietary supplement; ss.  
XX  
OS Euglena gracilis.  
XX  
FH Key Location/Qualifiers  
CDS 14..1273  
FT /\*tag= a  
FT /transl\_except= (pos:71..75, aa:ValSerAlaTrp)  
FT /product= Fatty\_acid\_delta-8\_desaturase  
XX  
FN WO200034439-A1.  
XX  
PD 15-JUN-2000.  
XX  
PF 06-DEC-1999; 99WO-US28655.  
XX  
PR 07-DEC-1998; 98US-0111301.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Browse JA, Wallis JG, Watts JL;

Pythium irregulare  
C. purpureus delta  
C. purpureus delta  
B. napus sld1 DNA.  
Wheat sphingolipid  
Soybean sphingolipid  
Sphingolipid desat  
C. purpureus delta  
C. purpureus delta  
Arabidopsis thalia  
Arabidopsis thalia  
A. thaliana sld1 D  
Florida bitterbush  
Human cDNA sequenc  
Arabidopsis thalia  
Borage delta-6 des  
Borage delta-6 des  
Borage delta-6 des  
DNA encoding Bora  
Human cDNA clone  
Human delta-6-des  
Human breast and o  
Human polynucleoti  
Contig 2511785 enc  
Human desaturase g  
Contig 2511785 enc  
Human delta-5-des  
Human contig DNA e  
Nucleotide sequenc  
Contig 2535 encodi  
Human desaturase g  
Contig 2535 encodi  
Human delta-5-des  
Human contig DNA e  
Nucleotide sequenc

XX  
DR WPI: 2000-431293/37.  
DR P-PSDB; AAY96722.  
XX  
PT Purified protein having desaturase activity, useful for creating a  
PT double-bond between two carbons  
XX  
PS Claim 8; Fig 7B; 74pp; English.  
XX  
CC This cDNA encodes Euglena gracilis fatty acid delta-8 desaturase.  
CC The sequence is useful for recombinant production of the enzyme and for  
CC generating transformed host cells and transgenic plants. The desaturase  
CC can be used for creating a double-bond between two carbons. In  
CC particular, the enzyme is useful for producing polyunsaturated fatty  
CC acids and for generating enzyme-specific antibodies useful for  
CC identifying desaturases. Oil-seed plants may be engineered to incorporate  
CC the enzyme, so that the plants produce seed oil rich in fatty acids. The  
CC fatty acids could be incorporated usefully into infant formula, foods of  
CC all kinds, dietary supplements, nutraceutical and pharmaceutical  
CC formulations.  
XX  
SQ Sequence 1275 BP; 294 A; 326 C; 327 G; 328 T; 0 other;  
Query Match 100.0%; Score 1275; DB 21; Length 1275;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATTTTTCGAAATGAAGTCAAGCGCAAGCGCTATCCCTTACAATTGATGAACA 60  
Db 1 ATTTTTCGAAATGAAGTCAAGCGCAAGCGCTATCCCTTACAATTGATGAACA 60  
QY 61 ACATATGATGGTCAATTCACCTCGTGGCGGAATATAGAGAAATACCAAG 120  
Db 61 ACATATGATGGTCAATTCACCTCGTGGCGGAATATAGAGAAATACCAAG 120  
QY 121 AAGGGATGCCACTGATGCTTCAATGTTATGCACTTTCAAGAACCTTCGACAGCTCAA 180  
Db 121 AAGGGATGCCACTGATGCTTCAATGTTATGCACTTTCAAGAACCTTCGACAGCTCAA 180  
QY 181 GGGCATGCCCAAAATCAATCCAGTTTGTAGTTGCCACCCAGCTGCAGTGAATGAAC 240  
Db 181 GGGCATGCCCAAAATCAATCCAGTTTGTAGTTGCCACCCAGCTGCAGTGAATGAAC 240  
QY 241 TCAAGAGGATTTCCGGAAGCTCCGAGAAGTTGATCGCACTGGCATGTTTGCATGCTC 300  
Db 241 TCAAGAGGATTTCCGGAAGCTCCGAGAAGTTGATCGCACTGGCATGTTTGCATGCTC 300  
QY 301 CCCCCTCTGTTACTATACAAAATCAGCACACACACACACACACACACACACACACAC 360  
Db 301 CCCCCTCTGTTACTATACAAAATCAGCACACACACACACACACACACACACACACAC 360  
QY 361 CTTGATGGTTCAGTATCAGATGATTTTATGTTGGGAGTGTGCTGGGATGCACTATCA 420  
Db 361 CTTGATGGTTCAGTATCAGATGATTTTATGTTGGGAGTGTGCTGGGATGCACTATCA 420  
QY 421 ACAGATGGGCTGGCTTTCATCAGATTTCCACACACACACACACACACACACACAC 480  
Db 421 ACAGATGGGCTGGCTTTCATCAGATTTCCACACACACACACACACACACACACAC 480  
QY 481 GAACAACTTCGTTGGGACTGGTATTTGGCAATGCTGCAAGTTTTCCTGATGATGTTG 540  
Db 481 GAACAACTTCGTTGGGACTGGTATTTGGCAATGCTGCAAGTTTTCCTGATGATGTTG 540  
QY 541 GAAGGACAGACAAATGCATATTCGGCAACCAATGTTCAAGGGCAGCACCTGATAT 600  
Db 541 GAAGGACAGACAAATGCATATTCGGCAACCAATGTTCAAGGGCAGCACCTGATAT 600  
QY 601 TGACAACTTCCTCCCTTACCTGCTGAGGATGAGCTCACAGGGCGTACCGATTC 660  
Db 601 TGACAACTTCCTCCCTTACCTGCTGAGGATGAGCTCACAGGGCGTACCGATTC 660  
QY 661 CGCAGAGCTCAATTCAGTCCAGCAGTACTATTTCTGGTATCTGATCTGTTGGGTT 720  
Db 661 CGCAGAGCTCAATTCAGTCCAGCAGTACTATTTCTGGTATCTGATCTGTTGGGTT 720

Db 661 CCGAAGCTCATTCAGTCCAGCAGTACTATTTCTTGGTCACTGTATCTTGTGGGTT 720  
QY 721 CATTTGGTGTTCAGTGCCTGTTGACCGTGGCAGTGTGAAAGACAGAGATACCAATT 780  
Db 721 CATTTGGTGTTCAGTGCCTGTTGACCGTGGCAGTGTGAAAGACAGAGATACCAATT 780  
QY 781 CTATCGCTCTCAGTATAGAAGAGGACCATTTGGCTCGCCCTGCACCTGGACCTTCAAGGC 840  
Db 781 CTATCGCTCTCAGTATAGAAGAGGACCATTTGGCTCGCCCTGCACCTGGACCTTCAAGGC 840  
QY 841 CTTGTTCCACTTATTTTATGCCAGCATCTCCATCGCTGTGTTGTTGTTGTTGTTGTTGTT 900  
Db 841 CTTGTTCCACTTATTTTATGCCAGCATCTCCATCGCTGTGTTGTTGTTGTTGTTGTTGTT 900  
QY 901 GGAGCTGGTGGCGCTTCGGCATTTGGCATTTGGCATTTGGCATTTGGCATTTGGCATTT 960  
Db 901 GGAGCTGGTGGCGCTTCGGCATTTGGCATTTGGCATTTGGCATTTGGCATTTGGCATTT 960  
QY 961 GAAGATCGGGGACCCAGCTCTGGGATGGCCATGATTTCTCGGTTGGCCAGATCCATGAGAC 1020  
Db 961 GAAGATCGGGGACCCAGCTCTGGGATGGCCATGATTTCTCGGTTGGCCAGATCCATGAGAC 1020  
QY 1021 CATGACATTCGGCGAGGATTTATCACAGATTTGTTTTTCGGAGGCTTGAATTAACAGAT 1080  
Db 1021 CATGACATTCGGCGAGGATTTATCACAGATTTGTTTTTCGGAGGCTTGAATTAACAGAT 1080  
QY 1081 TGAGCACCATTGTTGGCGGACCTCCCTCGCCACAACTGACAGCGGTTAGCTACCAGGT 1140  
Db 1081 TGAGCACCATTGTTGGCGGACCTCCCTCGCCACAACTGACAGCGGTTAGCTACCAGGT 1140  
QY 1141 GGAACAGCTCTGCGCAGAACACAACTCGCGTATCGGAACCCGCTGCCCATGAAGGTT 1200  
Db 1141 GGAACAGCTCTGCGCAGAACACAACTCGCGTATCGGAACCCGCTGCCCATGAAGGTT 1200  
QY 1201 GGTATCCTCTGCGCTATCTGCGGCTGTTGCGCCGATGCGGAGAGAACCCGCGG 1260  
Db 1201 GGTATCCTCTGCGCTATCTGCGGCTGTTGCGCCGATGCGGAGAGAACCCGCGG 1260  
QY 1261 GAAGGCTCTATAAGG 1275  
Db 1261 GAAGGCTCTATAAGG 1275  
RESULT 2  
AAZ47129  
ID - AAZ47129 standard; DNA; 1374 BP.  
XX  
AC AAZ47129;  
XX AC  
XX AC  
DT 28-MAR-2000 (first entry)  
XX  
DE Fungal delta6-desaturase coding sequence.  
XX  
XX Polyunsaturated fatty acid; fungus; delta6-desaturase; animal feed;  
XX transgenic animal; malnutrition; biosynthesis; ds.  
XX  
XX Unidentified.  
XX OS  
XX WO9961602-A1.  
XX PN  
XX 02-DEC-1999.  
XX PD  
XX 28-MAY-1999; 99WO-US12088.  
XX PF  
XX 29-MAY-1998; 98US-0087578.  
XX PR  
XX (OHIS ) UNIV OHIO STATE.  
XX PA  
XX Kopchick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;  
XX PI WPI: 2000-072619/06.  
XX DR P-PSDB; AAY56045.  
XX DR  
XX XX

QY 394 GGCAGTGTGCTTGGGATGCACCTATCAACAGATGGGCTGGCTTCTCATGACATTTGCCA 453

468 GCGTGGCTTTTGGGCTCTGTTGCGCAGCAGTGGATGGTGGCTCAGCACTTTTGCA 527  
 454 CCACGAGACTTTCAAGAACCGGAACTGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513  
 528 TCACGAGCTTTCCAGGACCGTTCTGCGGTGATCTTTTGGGGCCCTTCTTGGGAGGTGT 587  
 514 TCTGCAAGGTTTTTCCGTCACATGTTGGAAGGAGCAGACACATGCAATCTCGCAAC 573  
 588 CTGCCAGGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 647  
 574 CAATGTTCAAGGCGCAGCAGCTGATATTGACACCTCCGCCCTTAGCTGCTGCTGCTG 633  
 648 CACGCTCCAGCGGAGGATCCGACATGACACCCACCTCTCTGACCTGGAGTGAACA 707  
 634 T-----GACGTCACACGGGGCTCACCGATTTCCGCAAC 666  
 708 TCGTTGGAGATGTTCTCGGATGTCAGATGAGGAGCTGACCCGATGCTGCTGCTGCT 767  
 667 GCTCATTCAGTCCAGCAGTACTATTCTTGGTCACTGATCTTCTTGGGTTCAATTTG 726  
 768 CATGGTCTGAACCACTGCTGTTTACCTCCCATCTCTGCTTGGCGGCTCTCTCCCTG 827  
 727 GTGTTTCCAGTGGCTGTTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780  
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 1008 GCAGGCGGTGGGGAATCTTGGGATCGTGGTTCGCTCAACCAACGATGCTGCTG 1067  
 961 GAAGATCGGGGACCCAGTCTGGGATGCGGATGCGGATGCTGCTGCTGCTGCTGCTG 1020  
 1068 TGTGATCTCGAAGGAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATG 1127  
 1021 CATGAACATTCGCGAGGATTTATCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 1128 TGTGATGTCACCCCGGCTTATTTGCCAACTGGTTCACGGGTGATTTGAACATCATGAT 1187  
 1081 TGAGCACCATTGTTGGCGGACCTCCCTCGCCCAACCTGACAGCGGTTAGCTACCAAGT 1140  
 1188 CGAGCACCATTGTTCCCTTCGATGCTCGCCCAACTTTTCAAGATCCAGCTGCTGT 1247  
 1141 GGACAGCTGTGCGAAGCAGACACCTGCGGATTCGGAACCC 1182  
 1248 CGAGACCCCTGTGCAAAAGTACATGTCGATATCCACACAC 1289

RESULT 4

AA63624  
 ID AA63624 standard; cdna; 1617 BP.

AC  
 XX  
 XX  
 XX

15-FEB-1999 (first entry)

DE  
 DE  
 DE  
 DE

KW  
 KW  
 KW  
 KW  
 KW  
 KW  
 KW

Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;  
 malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 cholesterol level; endometriosis; premenstrual syndrome;  
 myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

OS Mortierella alpina.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 71..1444  
 FT /\*tag= a  
 FT /product= delta-6 desaturase  
 XX  
 PN W09846763-A1.  
 XX  
 XX 22-OCT-1998.  
 XX  
 XX 10-APR-1998; 98WO-US07126.  
 XX  
 XX 11-APR-1997; 97US-0834655.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX (CALJ ) CALGENE LLC.  
 XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
 XX Thurmond J;  
 XX WPI; 1998-594582/50.  
 XX P-PSDB; AAW841137.  
 XX  
 XX New isolated fatty acid desaturase enzymes - used for the production  
 of polyunsaturated fatty acids for use in, e.g. pharmaceutical  
 compositions, nutritional compositions, cosmetics or animal feed  
 Claim 1; Fig 3A-E; 165pp; English.  
 XX  
 XX The present sequence encodes a Mortierella alpina fatty acid delta-6  
 desaturase enzyme. The enzyme sequence is used in the methods of  
 the invention. The specification describes methods for desaturating a  
 fatty acid and for producing a desaturated fatty acid by expressing  
 increased levels of a desaturase. The present desaturase is an enzyme  
 which introduces a double bond carbons 6 and 7 from the carboxyl end of  
 a fatty acid molecule. The enzyme can be used for desaturating fatty  
 acids. The enzyme can be used to produce polyunsaturated fatty acids,  
 which can be used for treating malnutrition, in pharmaceutical  
 compositions, in cosmetics or in animal feed. The polyunsaturated fatty  
 acids can be used for treating e.g. restenosis after angioplasty,  
 inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes  
 or eczema or reduce blood pressure. They can also be used to inhibit  
 platelet aggregation, cause vasodilation, lower cholesterol levels,  
 inhibit proliferation of vessel wall smooth muscle and fibrous tissue,  
 reduce or prevent gastro-intestinal bleeding and other side effects  
 caused by non-steroidal anti-inflammatory drugs, prevent or treat  
 endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis  
 and chronic fatigue after viral infections, treat AIDS, multiple  
 sclerosis, acute respiratory syndrome, hypertension and inflammatory skin  
 disorders.  
 XX  
 SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;

Query Match 9.5%; Score 121.6; DB 19; Length 1617;  
 Best Local Similarity 49.38; Pred No. 9.4e-27;  
 Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;  
 Qy 394 GGCAGTGTGCTGGGATGCACATCAACAGATGGCTGGCTTCTCATGACATTTGCCA 453  
 Db 538 GGCTGCGCTTTTGGTCTGTTCTGGCAGCAGTGGGATGTTGGCTCAGCACTTTTGCA 597  
 Qy 454 CCACGACACTTCAAGAACCGGAACTGGAACAACTCTGGGACTGGTATTTGGCAATGG 513  
 Db 598 TCACCAAGTCTTCCAGGACCGCTTCTGGGGTGATCTTTTCGGGCGCTTCTTTGGGAGGTGT 657  
 Qy 514 TCTCAGAGTGTTCCTGACATCTGGAAGCAGACACATGACACATTCATTCGCAAC 573  
 Db 658 CTGCGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717  
 Qy 574 CAATGTTCAAGGGCAGCAGCCTGATATATGACAACTCCCGCTTAGCTGTGCTGAGGA 633  
 Db 718 CAACGTCACGGCAGGATCCGACATTTGACCCACCTCTGTTGACCTGGAGTGAGCA 777



QY 727 GTGTTTCCAGTCCGTTGACCGTGC-----CGAGTTTGAAGGACAGAGATAACCAATT 780  
 DB 898 GTGCTCCAGTCCATCTCTTTGCTGCTAAGGTCAGGCCCAACACCCCTCGGGCCG 957  
 QY 781 CTATCGCTCTCAGTATAGAAGAGGCCATTGGCTCGCCCTGCACTGGACCTTGAAGGC 840  
 DB 958 GCGTGTGCCCATCTCGTTGGTCGAGCAGCTGCTGCTGGCATGCACTGGACCTGGTACCT 1017  
 QY 841 CCGTGTCCACTTATCTTTATGCCAGCATCTCAGATCGCTGTTGGTGTCTTTTCGTTTC 900  
 DB 1018 CCCCACCATGTTCTCTTATCAAGGATCCCGTCAACATGCTGCTGTTACTTTTGGTGTG 1077  
 QY 901 GGAGCTGTTGGCGGCTCGCATTCGATTCGATTCGTTGTTTCATCAACCACTACCCACTGGA 960  
 DB 1078 GCAGCGGTGTCGGGAACTTGTGGGATCGTGTCTCGCTCAACCAACAGGATGCGC 1137  
 QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATGATTCCTCGTTGGCCAGATCCATGAGAC 1020  
 DB 1138 TGTGATCTCGAAGGAGGAGCGGTCGATATGATTTCTTCAAGACGATCATCACGGG 1197  
 QY 1021 CATGACATTCGGCGAGGATATACAGATTTGTTTTCGAGGCTTGAATACAGAT 1080  
 DB 1198 TCGTATGATTCACCCCGGCTTATTTGCCAACTGGTTACGCGGTGATTTGAATATCAGAT 1257  
 QY 1081 TGAGCACCATTGTTGGCCGACCTCCCTCGCCACACCTGACAGCGGTTAGTACCAGGT 1140  
 DB 1258 CGAGCACCATTGTTCCCTTCGATGCTCGCCACACACTTTTCAAGATCCAGCTGCTGT 1317  
 QY 1141 GGAACAGCTGTCCCAAGACACAACTGCGGTATCGGAACCC 1182  
 DB 1318 CGAGACCTGTGCAAAAGTACAATGTCGGATACCAACAC 1359

RESULT 6

AAA09430  
 ID AAA09430 standard; DNA; 1617 BP.  
 AC AAA09430;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE M. alpina delta-6, fatty acid desaturase coding sequence.  
 KW delta-6 desaturase; gamma-linolenic acid; biosynthesis;  
 KW transgenic insect cell; polyunsaturated long chain fatty acid;  
 KW antiinflammatory; antirheumatic; antidiabetic; antipsoriatic;  
 KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;  
 KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;  
 KW antiaggregant; vasotrophic; ss.  
 XX  
 OS Mortierella alpina.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 71..1443  
 FT /\*tag= a  
 FT /\*product= delta-6\_desaturase  
 XX  
 PN WO200020602-A2.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 29-SEP-1999; 99WO-US22686.  
 XX  
 PR 05-OCT-1998; 98US-0103110.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Mukerji P, Huang Y, Parker-barnes JM, Das T;  
 XX  
 DR WPI; 2000-328935/28.  
 DR P-PSDB; AAY92599.  
 XX  
 PT Novel transgenic insect cells comprising a nucleotide sequences which

PT encode delta-6-desaturase or delta-12- desaturase, useful for producing  
 PT poly-unsaturated long chain fatty acids, e.g. arachidonic acid  
 XX  
 PS Example 2; Page 144-145; 170pp; English.  
 XX  
 CC The fatty acid desaturases are able to catalyze the conversion of oleic  
 CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of  
 CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells  
 CC comprising a nucleotide sequence which encodes a polypeptide comprising  
 CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6  
 CC desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are  
 CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated  
 CC from the recombinant insect cells are also claimed. Production of  
 CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many  
 CC advantages, as insect cells have greatly simplified lipid compositions,  
 CC are not subject to external variable fluctuations, and can easily be  
 CC maintained and manipulated. The oils are used in pharmaceutical  
 CC compositions, infant formulas, dietary supplements or substitutes, and  
 CC cosmetics (all claimed). The PUFA supplements have antinflammatory,  
 CC antirheumatic, antidiabetic, antipsoriatic, osteopathic, cytostatic,  
 CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,  
 CC hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic  
 CC activity.  
 XX  
 SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;  
 Query Match 9.5%; Score 121.6; DB 21; Length 1617;  
 Best Local Similarity 49.3%; Pred. No. 9.4e-27;  
 Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;  
 QY 394 GCGAGTGTGCTTGGGATGCACATATCAACAGATGGGTGCTTCTCATGACATTTGCCA 453  
 DB 538 GCGTGGCTTTGGGTCTGTTGGGAGCAGTGGGATGGTGGCTCACACATTTTGGCA 597  
 QY 454 CCACAGACTTTCAAGAACCGGAACCTGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513  
 DB 598 TCACCAAGGTCTTCAGGACCGTTTCTGGGTGATCTTTTCGGCGCTCTTTGGAGGTG 657  
 QY 514 TCTGCAAGTGTTCGTCGATGATTTGGGAGGACAGACAAATGCACATCATTCGGCAAC 573  
 DB 658 CTGCCAGGCTTCTCTGCTCTGCTGGTGGAGGACAAACACACTCACCGCGCGCCC 717  
 QY 574 CAATGTTCAAGGACGACGCTGATATTGACACCTCCCCCTTACCTGGTCTGAGGA 633  
 DB 718 CACGTCACGCGGAGGATCCGACATTCACACCCCTCTGTTGACCTGGATGAGCA 777  
 QY 634 T-----GACGTACACAGCGGCTGACCGATTTCCCGCAA 666  
 DB 778 TCGTGTGGAGATGTTCTCGGATGTCAGATGAGGAGCTGACCGCATGTGGTCGCTTT 837  
 QY 667 GCTCATTCAGTTCACGACGATCTATTTCTGTCATCTGTATCTTGTGGTTCATTG 726  
 DB 838 CATGTCCTGAACACGACGCTGTTTACTTCCCTTCTCTCTGCTGCTGCTCTCTCTG 897  
 QY 727 GTGTTTCCAGTGGTGTGACCGTGC-----GCAGTTTCAAGGACAGAGATAACCAATT 780  
 DB 898 GTGCTCCAGTCCATCTCTTTGTGCTGCTAAGGTCAGGCCCAACAGCCCTCGGCGC 957  
 QY 781 CTATCGCTCTCAGTATAGAAGAGGCCATTTGGCTCGCCCTGCACTGGACCTTGAAGGC 840  
 DB 958 GCGTGTGCCCATCTCGTTGGTCGAGCAGCTGCTGCTGGCATGCACTGGACCTGGTACCT 1017  
 QY 841 CCGTGTCCACTTATCTTTATGCCAGCATCTCAGATCGCTGTTGGTGTCTTTTCGTTTC 900  
 DB 1018 CGCCACCATGTTCTCTTTCATCAAGGATCCCGTCAACATGCTGCTGTTACTTTTGGTGT 1077  
 QY 901 GGAGCTGTTGGCGGCTTCGGCATTCGATTCGATTCGTTTTCATGAACCACTACCCACTGGA 960  
 DB 1078 GCAGCGGTGTCGGGAACTTGTGGGATCGTGTCTCGCTCAACCAACAGGATGATGCC 1137  
 QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATGATTTCTCGTTGGCCAGATCCATGAGAC 1020  
 DB 1138 TGTGATCTCGAAGGAGGCGGTTCGATATGGATTTCTTCCAGGACGATCATCACGGG 1197



QY 1021 CATGAACATTCCGGAGGGATTATACAGATTGGTTTTTCGGAGGCTTGAATACAGAT 1080  
 Db 1198 TCCTGATGTCACCGGGTCTATTTGCCAACTGGTTCACGGGTGGATTGAACATACAGAT 1257  
 QY 1081 TGAGCACCAATTTGTGGCGGACCTCCCTCCGCCCAACCTGACAGCGGTTAGCTACCAAGT 1140  
 Db 1258 CGAGCACCACTGTCTCCCTTCGATGCTCCGCCCAACCTTTTCAAGATCCAGCGTGTGT 1317  
 QY 1141 GGAACAGCTGTCAGAGGACACAACTGCGCTGATGCGAACC 1182  
 Db 1318 CGAGACCTGTGCAAAAGTACAAATGTCGATACCCACACAC 1359

RESULT 7

AAAX76589

ID AAX76589 standard; cDNA; 1463 BP.

XX AC AAX76589;

XX DT 11-AUG-1999 (first entry)

XX DE Caenorhabditis elegans Delta 6 desaturase Ced6.1 encoding cDNA.

XX KW Caenorhabditis elegans; C. elegans; Delta 6 desaturase; Ced6.1;  
 KW gamma-linolenic acid; GLA; plant fatty acid; octadecatetraenoic acid;  
 KW OTA; eicosanoid; eczema; mastalgia; atherosclerosis; coronary disease;  
 KW hypercholesterolemia; diabetic neuropathy; viral infection; acne;  
 KW hypertension; cirrhosis; cancer; ss.

XX OS Caenorhabditis elegans.

XX FH Key Location/Qualifiers

XX FT CDS 11..1342

XX FT /\*tag= a

XX PN W0927111-AL.

XX PD 03-JUN-1999.

XX PF 24-NOV-1998; 98WO-GB03507.

XX PR 24-NOV-1997; 97GB-0024783.

XX PA (UYBR-) UNIV BRISTOL.

XX PI Napier JA;

XX DR WPI; 1999-370905/31.

XX DR P-PSDB; AAY17751.

XX PT Desaturase enzymes, the genes encoding them and their uses

XX PS Claim 29; Fig 1; 44pp; English.

CC The present sequence encodes Caenorhabditis elegans Delta 6 desaturase,  
 CC designated Ced6.1. Desaturase enzymes (I) may be used as immunogens to  
 CC raise and select antibodies (which may be used in immunoassays, and  
 CC diagnostic tests to detect the presence of (I) in a sample, or to purify  
 CC (I)) or as a selectable marker for transformation, especially  
 CC transformations involving plants. (I) can be used to produce gamma-  
 CC linolenic acid (GLA) (and derivatives of it), which is a high value  
 CC plant fatty acid that is widely used in medicine for the preparation of  
 CC compositions for treating disorders associated with deficiencies in GLA  
 CC or deficiencies in metabolites derived in vivo from GLA, such as  
 CC octadecatetraenoic acid (OTA) and eicosanoids. Disorders that may be  
 CC treated with GLA and OTA include eczema, mastalgia, atherosclerosis,  
 CC hypercholesterolemia, coronary disease, diabetic neuropathy, viral  
 CC infections, acne, hypertension, cirrhosis and cancer. The nucleotide  
 CC sequences (II) encoding (I) may be used as probes or primers. Probes may  
 CC be used to identify and purify nucleic acids and so may be used in  
 CC diagnosis to detect the presence of (II) in a sample. Primers are useful  
 CC for amplifying DNA by polymerase chain reaction (PCR). (II) may also be

CC used to prepare an organism that is either chill resistant or that  
 CC accumulates GLA or metabolites derived from GLA. Hybridizing DNA  
 CC molecules may be used as anti-sense molecules to alter the expression of  
 CC (II) by binding to it and preventing transcription. Hybridizing  
 CC molecules may also be provided as ribozymes which regulate expression by  
 CC cleaving RNA molecules.

XX Sequence 1463 BP; 445 A; 288 C; 277 G; 453 T; 0 other;

QY Query Match 8.8%; Score 112.8; DB 20; Length 1463;  
 Db Best Local Similarity 48.3%; Pred. No. 4.8e-24;  
 QY Matches 389; Conservative 0; Mismatches 402; Indels 15; Gaps 2;

QY 382 GTATTTTCATTTGGGCGAGTGTCTGGATGCATATCAACAGATGGCTGGCTTCTCA 441  
 Db 454 GTATATTACTTCTGCATGTTTATTAGCACTTGGCAAAATTCGGATGGTTAACACA 513  
 QY 442 TGACATTTGGCACCCACAGACTTTCAAGAACCGGAACCTGGAAACACCTCGTGGGACTGT 501  
 Db 514 TGAGTTCTGCCATCAACAGCAACAAAGACAGACCTTGAATGATATACTATTCTTGT 573  
 QY 502 ATTTGGCAATGGTCTCAAGGTTTTTCGTCGATGATTTGGAAGGACAGACAAATGACACA 561  
 Db 574 CTTTGGTAATTTCTTACAAGGATTTCAAGAGATTTGGTGAAGGACAAAGCATAACACTCA 633  
 QY 562 TCATTCGGCAACCAATGTTCAAGGGCAGCACCTGATATTTGACAAACCTCCCCCTTACC 621  
 Db 634 TCAGCTGCCACAAATGATTTGATCATGACGGGTGATTCGACTTGGCACCCTTTTCGC 693  
 QY 622 CTGCTCTGAGGATGACGTCACACGGGGTCAACCATTT-----CCCGCAAGCT 669  
 Db 694 ATTTATTCAGGAGATTTGTGCAAGTATAAGGCCAGCTTTGAAAAGCAATTCACAGAT 753  
 QY 670 CATTACGTTCCAGCAGTACTATTTCTTGGTCTCATCTGATCTTGTTCGGTTCATTTGGTG 729  
 Db 754 TGTACCATATCAACATCTCTATTTACCGCAATGCTTCCAATGCTCCCTTCTCATGGAC 813  
 QY 730 TTTCCAGTGGGTGTGACCGTGGCAGTTTCAAGGACAGATACCAATTTCTATCGCTC 789  
 Db 814 TGGTCAGTCAGTTCAATGGGTATTTCAAGAGATCAAAATGGAGTACAAGGCTATCAAG 873  
 QY 790 TCAGTATAAGAAAGGAGGCCATTGGCCTCGCCTGCACCTGGACCTTGAAGGGCCTCTTCCA 849  
 Db 874 AATGCAATTCGGGAGCAACAAATTTGTGGACATTTGGGCTT---GGGTATTTCTATCA 930  
 QY 850 CTTATCTTTTATGCCAGCATTCCTCACATCGCTGTGTGGTGTGTTTTTCGGTTCGAGCTGT 909  
 Db 931 ATTGTTCTTATTACCAACATGGCCACTTCGGGTTGCTTATTTCATTTATTTTACAAATGGG 990  
 QY 910 TGGCGGCTTCGGCATTTGGGATCGTGGTGTTCATGAACCACTACCCACTGGAGAGATCGG 969  
 Db 991 AGGAGGCTTTTGTGATGCTCAGCTAGTACATTTCAACCACTAACTCTGTGTGAATATCC 1050  
 QY 970 GGACCCAGTCTGGGATGGCCATGGATCTCGGTTGGCCAGATCCATGAGACCATCAACAT 1029  
 Db 1051 AGCCAAATTCGAATTTTAAACAATTCGCCGCTCTTCAAAATTTTGACCAACACGCAACAT 1110  
 QY 1030 TCGCGAGGAGGATTTACAGATTTGTTTTTCGGAGGCTTGAATTTACCAGATTTGACACCA 1089  
 Db 1111 GACTCCATCTCCATTCATTTGATTTGGGTTGGACTCAATTTATCATGATCGAGCACCA 1170  
 QY 1090 TTTGTGGCGGACCTCCCTCGCCCAACCTGACAGCGGTTAGCTACCAAGGTTGGAACAGCT 1149  
 Db 1171 CTTTCCCAACAATGCCACCTTGAATCTGAAATCTGCTGCTGAAATATGTGAAGAATG 1230  
 QY 1150 GTGCCAAGCAGCAACCTGCGGTATC 1175  
 Db 1231 GTGCANAAGAAATAATCTTCTTACC 1256

RESULT 8

AAAX86961

ID AAX86961 standard; cDNA; 1344 BP.



generating transformed host cells and transgenic plants. The desaturase can be used for creating a double-bond between two carbons. In particular, the enzyme is useful for producing polyunsaturated fatty acids and for generating enzyme-specific antibodies useful for identifying desaturases. Oil-seed plants may be engineered to incorporate the enzyme, so that the plants produce seed oil rich in fatty acids. The fatty acids could be incorporated usefully into infant formula, foods of all kinds, dietary supplements, nutraceutical and pharmaceutical formulations.

574 GGAACCTTATCGCTCGCTCGTGGCAACCGCTGGCAGGCTTCACGCTGCAGTGGTGG 633  
 542 AAGGACAGACACATGACATATTCGGCAACCAATGTTCAAG-----585  
 634 AAGAACAAGCACAACTGCAACGCGCTGCCGAACCTGCACAGCGCAAGGAGGAGGCG 693  
 586 -----GCACAGCCTGATATGACAACTCCCGCTTAGCTGCTGAGGATGAGCTC 640  
 694 TCCATCGGCGACCGGACATCGACACCATCGCGCTGCTGCGGTCTAAGGATGCG 753  
 641 ACAGGGG-----GTACCGATTTCCCGAAGCTTATCAGTTCACAGCACTACTATTC 694  
 754 CGAAGCGCTTCGAGTCGCGCACGCGCTTCCTCATCGCAACCGAGGCTTCTATAC 813  
 695 TTGGTCACTGATATGTTGGGCTTATTTGGTGTTCAGTGGCTGCTGAGGATGAGCTC 754  
 814 TCCCGCTGCTGCTGCTGCGCGCTGAGTGGCTGCGCAGCTGCTTCTTCTAGCTGTC 873  
 755 AGTTGAAGACAGAGATAACCAATCTATCGCTCTCAGTATAGAAAGGAGGCTATGGC 814  
 874 ACCGAGTTCCTGCTCGCTGCTTCGACAAGGTTCGAGTTCGACGCGGAGAGCGGCT 933  
 815 CTCGCCCTGACAGGACCTTGAAGGCGCTTTCACATTTATTTATGCCAGACCTC 874  
 934 CTGATCGTGCATACATCTGCAGCTCGCATCCGCTACTTCTGCAACATGAGCTGTT 993  
 875 ACATCGCTGTTGTTTTCGTTTCGAGCTGTTGGCGCTTCGCGCATTCGATCGTG 934  
 994 GAGGCGTGGCATACTTCTCTGTCGCGGCGCTTCGCGCTTTCGCTGCGCGCTGGT 1053  
 935 GTGTTTCAAGCACTACCTACCTGGAAGATCGGAGCAGCTGCGGATGGCATGGA 994  
 1054 TTCAATTTGGCCACAGCGATGCTGCTGACAGCGCGGACCAAG-----CCGAC 1107  
 995 TTCTCGGTTGGCAGATCCATGAGACCATGACCATTCGCGAGGATTTATCAGATGG 1054  
 1108 TTCTGCGAGCTGAGGTGACACGACGCGCAACATCGCGGCTCGGTATTCAGTGG 1167  
 1055 TTTTTCGAGGCTTGAATACCATGAGCACCATTGTCGCGGACCTCCCTCGGCAC 1114  
 1168 TCCAGCGGTGTTGAATCACTACAGATGACCATACCTGTTCCGCTGCTGCGCGCAC 1227  
 1115 AACCTGACAGCGGTAGCTACCGGTTGGAACAGCTGTCGAGAGCAACCTCCCTAT 1174  
 1228 AACTTGCACAGGTCAAGTGTCTCATCAAGTGTGATGACAGGATTCGACATCCCTC 1287  
 1175 CGGAACCGCTGCCCCATGAGGCTGCTCATCTGCTGCTGCTATCTGCGGCTTC 1231  
 1288 CAGGAGACCGGCTTCTGGGAGGCGATCTAGAGGTCTGAGGACCTGGCGGACATC 1344

RESULT 11  
 AAF25730  
 ID AAF25730 standard; DNA; 1467 BP.  
 XX AC AAF25730;  
 XX DT 06-APR-2001 (first entry)  
 XX DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 3.  
 XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;  
 KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;  
 KW cosmetic; ds.  
 XX OS Ceratodon purpureus.  
 XX FH Location/Qualifiers  
 FT CDS 10..1461  
 FT a  
 FT /product="delta6-acetylenase/delta6-desaturase"  
 XX

PN WO200075341-A1.  
 XX 14-DEC-2000.  
 PD 07-JUN-2000; 2000WO-EP05274.  
 XX 07-JUN-1999; 99DE-1025718.  
 PR 22-DEC-1999; 99DE-1062409.  
 XX (BADI ) BASF AG.  
 PA Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;  
 PI WPI; 2001-112150/12.  
 XX P-PSDB; AAB46436.  
 DR Nucleic acid encoding delta6-acetylenase or desaturase, useful for  
 XX producing plant oils with increased content of unsaturated fatty acids  
 PT  
 PT Claim 1a; Page 46-48; 69pp; German.  
 PS This invention describes a novel isolated nucleic acid (I) encoding  
 CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase  
 CC activity. The invention also describes (a) amino acid sequences encoded  
 CC by (I); (b) an expression cassette (EC) containing (I) linked to one or  
 CC more regulatory sequences; (c) a vector containing (I) and EC; (d)  
 CC organisms containing (I), EC or the vectors of (c); (e) preparation of  
 CC unsaturated fatty acids (A) or triglycerides (TG) with increased content  
 CC of (A) by introducing (I) or EC into an oil-producing organism; (f)  
 CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by  
 CC method (g). (I) are used to produce transgenic plants (or other  
 CC organisms) that produce oils or triglycerides (TG) with increased content  
 CC of unsaturated fatty acids (A) and to isolate related sequences by  
 CC homology screening. (A), or TG containing them, are useful in human  
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and  
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,  
 CC can be used to suppress expression of (II), resulting in oils with  
 CC increased content of saturated fatty acids.  
 XX SQ Sequence 1467 BP; 356 A; 349 C; 379 G; 383 T; 0 other;  
 Query Match 5.6%; Score 71.6; DB 22; Length 1467;  
 Best Local Similarity 45.4%; Pred. No. 2.9e-11;  
 Matches 352; Conservative 0; Mismatches 409; Indels 15; Gaps 2;  
 Qy 401 TTGCTGGGATGCACTATCAACAGATGGCTGGCTTTCTCATGACATTTGCCACACGAG 460  
 Db 604 TTGATGGTCTCTTCGTCACACAGTGTGGATGGCTTGGCCATGATTTCTTTCATCAACAG 663  
 Qy 461 ACTTTCAGAACCGGAAGTGAACACCTCTGGGAGCTGGTATTTGGCAATGGTTCGCA 520  
 Db 664 GTCTTTGAGAACCCGTACCGGCAACTCTCTTTGGCTATTTGTCGGAATTTGCGTGT 723  
 Qy 521 GGTTTTCCGTTGACATGTTGGAAGGACAGACACATGCAATCTCTCGGCAACCAATGTT 580  
 Db 724 GGCTTTAGTATCATGTGGAGGACGAGACACATTCATCATCTGCTCCGATGAG 783  
 Qy 581 CAAGGCGACGACCTGATATTGACAACCTCCCGCTTTAGCTGCTGAGATGACGCTC 640  
 Db 784 TCGCAGCAACAGTACACACCTTAGACGAAGACATTTGATCTCTCCCATCATTTCCCTGG 843  
 Qy 641 ACAGGGGCTGACCGATTTCCCGCAAGCTATTGATGTTCCAGCAGTACTATTTCTTGGTC 700  
 Db 844 AGCAAGGAATTTTGGCCACCGTTGAGAGCAAGAGAAATTTCCGAGTCTCTCAATATCAG 903  
 Qy 701 ATCTGTATCTGTTGCGGTTTCATTTGGTGTTCCTCCAGTCCGTTGTCACCTGCGCAGTTG 760  
 Db 904 CACTACATGATTTCTGCTCTATTGTTATGCGCCGGTACAGTTGAGCTTTTGGAAAGTTG 963  
 Qy 761 AAGGACAGAGATAACCAATTTCTATCGCT---CTCAGTATAAGAGGAGGCCATTTGGCCTC 817

Db 964 CTCTTCATTCATCTGATTTGAGCAGCAGCAGGATTTAGAGAGGGAACAGTT 1023  
QY 818 GCCTTGACATGGACCTTGAAGGCCCTTTCCACTTATTTATGATCCCATCTCACA 877  
Db 1024 GCTTTTTCACATGCGCTGTTGAGTGGCTGCGTTCCATATTTTGGCGGGTGCCTAAG 1083  
QY 878 TCCTGTTGTTGTTTTCGTTTCGGAGCTGTTGGCGGCTTCGCGATTCGATCGTGGTG 937  
Db 1084 CTTCTGCGTGGATGGTAGCACTGAGCTTGTGGCGGTTGTTGTTGGGATTCGTTT 1143  
QY 938 TTCTATGACCACTACCCACTGGGAGAGATCGGGAGCCAGCTGCTGGATGGCAATGGATTC 997  
Db 1144 ACCTTGATCACAATGGAAGGATTTTACATGAATCG-----AAGACTTC 1191  
QY 998 TCCTGTTGCGAGATCCATGAGACCAATGAGCAATTCGCGAGGATTTATCAGATTTGTTT 1057  
Db 1192 GTGAGAGCCAGGTTATTACCAACCGTAACACCAAGCGAGGCTGTTTCAAGATTGGTTC 1251  
QY 1058 TTCGGAGGCTTGATTTACCAATGAGCACCATTGTTGGCGGACCTTCCTCGCCACAAC 1117  
Db 1252 ACTGGGGGACTCGACACCCAGATTGAGCATCACTGTTTCCACAAATGCCAGGCACAAC 1311  
QY 1118 CTGACAGCGGTTAGCTACCAAGTGGAAACAGCTGTGCGAGAGCAACAACTGCCGTA 1173  
Db 1312 TACCCCAAGATCGCACTCAGGTCGAGGCTCTTTGCAAGAGCAAGCGCCTCGAGTA 1367

## RESULT 12

ID AAF25729  
XX AAF25729 standard; DNA; 2040 BP.  
AC AAF25729;  
XX  
XX  
DT 06-APR-2001 (first entry)  
XX  
DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 1.  
XX  
KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;  
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;  
KW cosmetic; ds.  
XX  
OS Ceratodon purpureus.  
XX  
FH Key Location/Qualifiers  
FT CDS 176..1627  
FT /tag= a  
FT /product= "delta6-acetylenase/delta6-desaturase"  
XX  
PN WO200075341-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 07-JUN-2000; 2000WO-EP05274.  
XX  
PR 07-JUN-1999; 99DE-1025718.  
PR 22-DEC-1999; 99DE-1062409.  
XX  
PA (BADI ) BASF AG.  
XX  
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaeheringer U;  
XX WPI; 2001-112150/12.  
DR P-PSDB; AAB46435.  
XX  
PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for  
PT producing plant oils with increased content of unsaturated fatty acids  
XX  
PS Claim 1a; Page 41-44; 69pp; German.  
XX  
CC This invention describes a novel isolated nucleic acid (I) encoding  
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase  
CC activity. The invention also describes (a) amino acid sequences encoded

CC by (I); (b) an expression cassette (EC) containing (I) linked to one or  
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)  
CC organisms containing (I), EC or the vectors of (c); (e) preparation of  
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content  
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)  
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)  
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by  
CC method (g). (I) are used to produce transgenic plants (or other  
CC organisms) that produce oils or triglycerides (TG) with increased content  
CC of unsaturated fatty acids (A) and to isolate related sequences by  
CC homology screening. (A), or TG containing them, are useful in human  
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and  
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,  
CC can be used to suppress expression of (II), resulting in oils with  
CC increased content of saturated fatty acids.

XX  
SQ Sequence 2040 BP; 528 A; 450 C; 505 G; 557 T; 0 other;

Query Match 5.6%; Score 71.6; DB 22; Length 2040;  
Best Local Similarity 45.4%; Pred. No. 3.5e-11;  
Matches 352; Conservative 0; Mismatches 409; Indels 15; Gaps 2;

QY 401 TTGCTTGGATGCACTATCAACAGATGGCTGGCTTTCTCATGACATTTGCCACCACAG 460  
Db 770 TTGATGGTCTCTTGGTCCAAACAGTGTGGTGTGCCCATGATTTCTTCATCAACAG 829  
QY 461 ACTTTTCAAGAACCCGAACTGGAACAACCTCGTGGGACTGGTATTTGGCAATGGTCTGCAA 520  
Db 830 GTCTTTGAGAACCGTACCGCACTCTCTTCTTGGCTATTTGTCGGCAATTTGCGTGCTT 889  
QY 521 GGTGTTTCCGTCATGTTGGAAGACAGACACAAATGCATCATTTGGCAACCAATGTT 580  
Db 890 GGCCTTAGTGTATCATGTGTGGAGCGAAGCAACAACTTCATCACTGCTCCGAATGAG 949  
QY 581 CAAGGACGACGACCTGATATTGACAACCTCCCGCTTGGCTGCTGAGGATGAGCTC 640  
Db 950 TGCAGCAACAGATGACACACCTCTAGACGAAGACATGTGATCTCTCCCATCATTTGCC 1009  
QY 641 ACAGCGCGCTCACCGATTTCCCGAAGCTCATTCAGTTCCAGCAGTACTATTTCTTGGTC 700  
Db 1010 AGCAAGGAATTTTGGCCACCGTTGAGAGCAAGAGAAATTTCCGAGTCTTCAATATCAG 1069  
QY 701 ATCTGTATCTTGTGGGTTTCATTTGGTGTTCAGTCGCGTGTTCACCGTGGCGAGTTTG 760  
Db 1070 CACTACATGATTTCTGCTCTATTGTTATGCGCGGTACAGTTGGATTTTGGAAAGTTG 1129  
QY 761 AAGGACAGAGATACCAATTTCTATCGCT--CTCAGTATAGAGAGGAGCCATTTGCCCTC 817  
Db 1130 CTCTTCATTCATCTGATTTGAGCAGCAGCAAGGATTTGATAGAGGGAACAGATT 1189  
QY 818 GCCCTGCACCTGGACCTTGAAGGCCCTGTTCACCTTATTTATGCCCAGCATCTCACA 877  
Db 1190 GCTTTTCACTACGCTGTTGAGTGGCTGCTTCCATATTTTCCCGGGTCTCGCTAAG 1249  
QY 878 TCCTGTTGTTGTTTTCGTTTCGAGCTGTTGGCGGCTTCGCGATTTGCGATTCGTTGGTG 937  
Db 1250 CCTCTGCTGGATGGTAGCAACTGAGCTTGTGCGCGGTTTGTGTTGGGATTCGTTT 1309  
QY 938 TTCTATGACCACTACCCACTGGAGAAAGATCGGGAGCCAGTCTGGGATGGCCATGGATTC 997  
Db 1310 ACCTTGAGTCACAATGGAAGGAGGTTTACATGAATCG-----AAGACTTC 1357  
QY 998 TCGGTTGGCCAGATCCCATGAGACCATGAACATTCGGGAGGAGGATTTATCAGATTTGGTTT 1057  
Db 1358 GTGAGAGCCAGGTTATTACCCCGTAACACCAAGCGAGGCTGGTGTCAAGATTTGGTTC 1417  
QY 1058 TTCGGAGGCTTGAATTACCAAGATTGAGCACCATTGTTGGCGGAGCCCTCCCTCGCCACAAC 1117  
Db 1418 ACTGGGGGACTCGACACCCAGATTGAGCATCACCTGTTTCCACAATATGCCAGGCACAAC 1477  
QY 1118 CTGACAGCGGTTAGTACCAGGTTGGAACAGCTGTGCCAGAGCAACAACTGCCGTA 1173  
Db 1478 TACCCCAAGATCGCACTCAGGTCGAGGCTCTTTGCAAGAGCAAGCGCCTCGAGTA 1533



PN W0200032790-A2.  
 XX 08-JUN-2000.  
 PD 02-DEC-1999; 99WO-US28589.  
 PF 03-DEC-1998; 98US-0110784.  
 PR (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;  
 XX WPI: 2000-412336/35.  
 DR P-PSDB; AAY71555.  
 XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing  
 PT transgenic plants and for producing antibodies specific to which is  
 PT useful for screening cDNA expression libraries  
 XX Disclosure; Page 48-49; 57pp; English.  
 XX The present sequence is a cDNA encoding sphingolipid desaturase  
 CC from clone wrel.pk0004.c7:fls isolated from wheat etiolated  
 CC seedling root cDNA library, wrel.  
 CC The present sequence is useful for producing  
 CC transgenic plants having altered levels of sphingolipid desaturase which  
 CC in turn would alter the fatty acid composition. The enzyme is useful  
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide  
 CC is also useful as primer or probe for screening cDNA libraries to  
 CC isolate desired full-length cDNA clones.  
 XX Sequence 1972 BP; 382 A; 516 C; 490 G; 484 T; 0 other;  
 SQ

Query Match 5.0%; Score 63.4; DB 21; Length 1972;  
 Best Local Similarity 44.6%; Pred. No. 1.2e-08;  
 Matches 348; Conservative 0; Mismatches 421; Indels 12; Gaps 2;

QY 405 TTGGGATGACTATACACAGATGGGTGGCTTCTCATGACATTTGCCACACACGACTT 464  
 Db TTTGCTTCTATCTGGATCCAGTCCGGGTGGATTTGCCATGACTCCGCCACCCACCAATCA 682  
 QY 465 TCAAGAACCGGAAGTTCGAGCAACCTCTGGGACTGGTATTGGCAATGCTCGAAGTT 524  
 Db CAGGACACCCCGGCTCAACCGCTCTCTGAGTGGTCTCCGGGAATGCTCACCGGCC 742  
 QY 525 TTCCGTGACATTTGGAAGGACAGACACAATCATCATTCGGCAACCAATGTTCAAG 584  
 Db TCGGCATCGCTGGTGGAGTTCAACACACACACACACACATCTCTGCAACAGCCTCG 802  
 QY 585 GGCACACCCCTGATATGACAACTCCGCCCTTAGCCTGGTCTGAGGATGACGTACAC 644  
 Db ACCATGACCCGGACCTCCAGCACTTCGCGCTCTTCGCGTTTCACCAAGCTCTTCAACA 862  
 QY 645 GGGCGTCACCGATTTCCGCAACCTCATTCAGTCCAGCAGTACTATTCTTGGTCACT 704  
 Db ACCTTTGGTGGTCTAGAGCGGACCTTGGCGTTTGGATGCCATATCAAGTTCTTCG 922  
 QY 705 GTATCTTGTGGCGTTTCAATTTGGTGTTCAGTGGCTGTGACCGTGGCGAGTTTGAAGG 764  
 Db TCAGCTACCAGCACTGGACATTTACCCGGTGTGGATTTGCAAGGATTAATCTTCTTG 982  
 QY 765 ACAGATATACCAATTTCTATCGCTCTCAGTATTAAGAAGGAGGCAATTTGGCCTCGCCCTGC 824  
 Db TGCAGTCAATCTGTCTTCTGATCAGCAAAAGAGGTGCGGACGCTTGGCTGGAGATCG 1042  
 QY 825 ACTGGACCTTGAAGCCCTGTTCACCTATTCTTTATGCCAGCATCTCATACGCTGT 884  
 Db CCGAGTTGACGGTTCTGGGTTTGGTATCCCTTGTCTGTCTTGGCTCCGAATTTGT 1102  
 QY 885 TGGTGTTTTCTGGTGGAGCTGTGGGGCTTCGCGCTTCGAGTTCGATCGT-----GG 935  
 Db 1103 GGGAGAGGTTGCTTTTGTGCTTGCATGCAAGCTTTGATGATCAGGGGATTCAGCATGTTCA 1162

QY 936 TGTTTCATGAACCACTACCACTGGAGAAGATCGGGGACCCAGTCTGGGATGCCCATGGAT 995  
 Db TCTGCTGAACCACTTCTCATCCGCTGTGTATGTTGGGCAC---CAAAGGGGAACCACT 1219  
 QY 996 TCTCGGTTGGCCAGATCCATGAGACCATTCGCGGAGGGGATTTATCAGAGATTGTT 1055  
 Db GGTTCAGAGGCAACACAGCGGCACACTTGATATCAAGTGTCTCCCGTGGATGGATTGTT 1279  
 QY 1056 TTTTCGGAGGCTTGAATTTACCAAGTTCAGCACCATTCTTGGCCGACCTCCCTCGCCACA 1115  
 Db TCCATGGTGTCTGAGTTCCAGTTCCAGTTGAACACCATTTCTTCTCGCCTCGCTCGCTGCC 1339  
 QY 1116 ACCTGACAGCGGTTAGTACAGGTGGGAACAGCTGTGCCAGAGCACAACTTCGCGTATC 1175  
 Db ACTATAGATGGTCGCGCGGATTTGCTGTGACCTTTTGCAGAGCATGGGCTGTCTTATG 1399  
 QY 1176 G 1176  
 Db 1400 G 1400

RESULT 15  
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 ID AAD01352 standard; cDNA; 1934 BP.  
 XX AAD01352;  
 AC AC  
 XX 12-OCT-2000 (first entry)  
 DT  
 XX Soybean sphingolipid desaturase cDNA #2.  
 XX Soybean; sphingolipid desaturase; membrane-bound desaturase;  
 KW transgenic plant; fatty acid; ss.  
 KW Glycine max.  
 OS  
 XX Key Location/Qualifiers  
 FT CDS 305..1657  
 FT /\*tag= a  
 FT /product= "Sphingolipid desaturase"  
 XX W0200032790-A2.  
 PN 08-JUN-2000.  
 PD 02-DEC-1999; 99WO-US28589.  
 PF 03-DEC-1998; 98US-0110784.  
 PR (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;  
 XX WPI: 2000-412336/35.  
 DR P-PSDB; AAY71554.  
 XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing  
 PT transgenic plants and for producing antibodies specific to which is  
 PT useful for screening cDNA expression libraries  
 XX Claim 2; Page 46; 57pp; English.  
 PS The present sequence is a cDNA encoding sphingolipid desaturase  
 CC from clone ssl.pk0017.b4:fls isolated from soybean seedling cDNA  
 CC library, ssl. The present sequence is useful for producing  
 CC transgenic plants having altered levels of sphingolipid desaturase which  
 CC in turn would alter the fatty acid composition. The enzyme is useful  
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide  
 CC is also useful as primer or probe for screening cDNA libraries to  
 CC isolate desired full-length cDNA clones.  
 XX Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;  
 SQ

Query Match 4.8%; Score 61.6; DB 21; Length 1934;  
 Best Local Similarity 57.1%; Pred. No. 4.3e-08;  
 Matches 112; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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QY	1045	CACAGATTGGTTTTTCGGAGGCTTGAATTACCAGATTGAGCACCATTTTGTGGCCGACCCCT	1104
Db	1396	GATGGATTGGTTTTTCGGTGGCTTGCAGTTTCAGCTTGAGCATCATTTTTCCTCAAGGCT	1455
QY	1105	CCCTGCCACAAACCTGACACGCGTTAGCTTACCAGGTGGAACACAGCTGTGCCAGAAGCACAA	1164
Db	1456	ACCTCGTGCCCAATTGAGGAAGATTTCGCCCTTGGTTAGTGACCTTTGCAAGAAGCATAA	1515
QY	1165	CCTGCCGATCGGAAC	1180
Db	1516	TTTGCCTTATAGGAGC	1531

Search completed: July 2, 2003, 13:38:13  
 Job time : 316.464 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 13:22:56 ; Search time 64.7752 Seconds  
(without alignments)  
6036.458 Million cell updates/sec

Title: US-09-857-583-3

Perfect score: 1275

Sequence: 1 attttttcgaatgaagt.....gcgggggaagctctataagg 1275

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121.6	9.5	1617	2	US-08-834-655-1
2	121.6	9.5	1617	3	US-08-834-033A-1
3	121.6	9.5	1617	3	US-09-363-374-1
4	121.6	9.5	1617	4	US-09-363-326-1
5	121.6	9.5	1617	4	US-09-330-235-17
6	51.8	4.1	1684	2	US-08-831-570-1
7	51.8	4.1	1684	2	US-08-831-575-1
8	51.8	4.1	1685	1	US-08-366-779-4
9	51.8	4.1	1685	1	US-08-789-936-4
10	51.8	4.1	1685	4	US-08-934-254-4
11	51	4.0	1686	4	US-09-439-261-6
12	51	4.0	1686	4	US-09-227-613-6
13	51	4.0	1843	4	US-09-439-261-7
14	51	4.0	1843	4	US-09-227-613-7
15	51	4.0	2257	4	US-09-439-261-8
16	51	4.0	2257	4	US-09-227-613-8
17	48.4	3.8	449	4	US-09-439-261-38
18	48.4	3.8	449	4	US-09-227-613-37
19	48.4	3.8	655	4	US-09-439-261-3
20	48.4	3.8	655	4	US-09-227-613-3
21	48.4	3.8	864	4	US-09-439-261-12
22	48.4	3.8	864	4	US-09-227-613-13
23	47.6	3.7	1702	4	US-08-934-254-26
24	45.6	3.6	473	4	US-09-439-261-37
25	45.6	3.6	473	4	US-09-227-613-36
26	45.6	3.6	1335	4	US-09-439-261-1
27	45.6	3.6	1335	4	US-09-227-613-1

28 44.8 3.5 918 4 US-09-439-261-5 Sequence 5, Appl  
29 44.8 3.5 918 4 US-09-227-613-5 Sequence 5, Appl  
30 44.8 3.5 960 4 US-09-439-261-36 Sequence 36, Appl  
31 44.8 3.5 960 4 US-09-227-613-35 Sequence 35, Appl  
32 44.8 3.5 990 4 US-09-439-261-35 Sequence 35, Appl  
33 44.8 3.5 990 4 US-09-227-613-34 Sequence 34, Appl  
34 41 3.2 6344 4 US-08-843-417-1 Sequence 1, Appl  
35 41 3.2 6524 4 US-08-669-656A-1 Sequence 1, Appl  
36 41 3.2 6527 4 US-08-669-656A-7 Sequence 7, Appl  
37 41 3.2 7052 4 US-08-669-656A-5 Sequence 5, Appl  
38 39.2 3.1 7218 1 US-08-232-463-14 Sequence 14, Appl  
39 35 2.7 428 4 US-09-397-787-246 Sequence 246, Appl  
40 33.8 2.7 4403765 4 US-09-103-840A-2 Sequence 2, Appl  
41 33.8 2.7 4411529 4 US-09-103-840A-1 Sequence 1, Appl  
42 33.6 2.6 2997 1 US-08-453-862-1 Sequence 1, Appl  
43 33.6 2.6 2997 2 US-08-452-734A-1 Sequence 1, Appl  
44 33.6 2.6 2997 4 US-08-176-401B-1 Sequence 1, Appl  
45 33.6 2.6 2997 5 PCT-US94-14989-1 Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-834-655-1  
; Sequence 1, Application US/08834655  
; Patent No. 5968809  
; GENERAL INFORMATION:  
; APPLICANT: KNUITZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,655  
; FILING DATE: 11-APR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RAE-VENTER, BARBARA  
; REGISTRATION NUMBER: 32,750  
; REFERENCE/DOCKET NUMBER: CGNE.124.00DS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 328-4400  
; TELEFAX: (650) 328-4477  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1617 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; US-08-834-655-1

Query Match 9.5%; Score 121.6; DB 2; Length 1617;  
Best Local Similarity 49.3%; Pred. No. 1.8e-28;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

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QY 394 GGCAGTGTTCCTGGGATGCATATCAACAGATGGCTGGCTTCTCATGACATTTGCCA 453
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QY 454 CCACCAAGCTTTCAAGAAGCGGAACATGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513
Db 598 TCACCAAGCTTTCAGGACCGTTTCGGGGTGATCTTCGGGGCCCTCTCTGGAGGTGT 657
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Db 658 CTGCCAGGCTTCTCGTCTCGTGGTGAAGGACAAAGCAGACATCACCACCGCCGCC 717
QY 574 CAATGTTCAAGGACGACCTCATATGACACCTCCGCCCTTAGCTGGTCTGAGGA 633
Db 718 CACGTCACGCGGAGATCCGACATGACACCCACCTCTGTGACCTGGAGTGAGCA 777
QY 634 T-----GACGTCACACGGGGCTCACCGATTTCCCGCAA 666
Db 778 TGGCTTGGAGATGTTCTCGGATGTCACAGATGAGGAGCTGACCCGATGTGGTCCGCTTT 837
QY 667 GCTCATCAGTTCACAGCTACTATTTCTGGTCATCTGTATCTTGTGGGTTTCAATTG 726
Db 838 CATGCTCTCAACAGCAGCTGTTTACTTCCCATCTCTCTGCTTGGCCGTCTCTCCTG 897
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QY 1021 CATGAACATTCGCGAGGATTAACAGATGCTGTTTTCGGAGGCTTGAATTAACAGAT 1080
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QY 1081 TGAGCACCATTCTGTGCGGACCTCCCTCGCCCAACCTGACAGCGGTAGCTACCAGGT 1140
Db 1258 CGAGCACCATTCTGTCCCTGATGCTTCCCAACTTTCACAGATCCAGCCTGCTGT 1317
QY 1141 GGAACAGCTGTGCGAAGCAGACACCTGCGGTATCGGAACC 1182
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RESULT 2

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US-08-834-033A-1
; Sequence 1, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTSON, DEBORAH
; APPLICANT: MURKIN, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LIMBACH AND LIMBACH, L. L. P.
; STREET: 2001 FERRY BUILDING

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; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-834-033A-1
;
; Query Match 9.5% Score 121.6; DB 3; Length 1617;
; Best Local Similarity 49.3%; Pred. No. 1.8e-28;
; Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;
;
; QY 394 GGCAGTGTTCCTGGGATGCATATCAACAGATGGCTGGCTTCTCATGACATTTGCCA 453
; Db 538 GGCCTGGCTTTTGGGCTGCTTTCGGCAGCAGTCCGGATGGTGGCTCAGCAGCTTTTGCA 597
; QY 454 CCACCAAGCTTTCAAGAAGCGGAACATGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513
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; Db 658 CTGCCAGGCTTCTCGTCTCGTGGTGAAGGACAAAGCAGACATCACCACCGCCGCC 717
; QY 574 CAATGTTCAAGGACGACCTCATATGACACCTCCGCCCTTAGCTGGTCTGAGGA 633
; Db 718 CACGTCACGCGGAGATCCGACATGACACCCACCTCTGTGACCTGGAGTGAGCA 777
; QY 634 T-----GACGTCACACGGGGCTCACCGATTTCCCGCAA 666
; Db 778 TGGCTTGGAGATGTTCTCGGATGTCACAGATGAGGAGCTGACCCGATGTGGTCCGCTTT 837
; QY 667 GCTCATCAGTTCACAGCTACTATTTCTGGTCATCTGTATCTTGTGGGTTTCAATTG 726
; Db 838 CATGCTCTCAACAGCAGCTGTTTACTTCCCATCTCTCTGCTTGGCCGTCTCTCCTG 897
; QY 727 GTGTTTCCAGTGGCTGTGACCGTGC-----GAGTTCGAAGGACAGAGATAACCAATT 780
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; QY 781 CTATCCTCTCAGTATAAAGAGGAGGCTTGGCCCTCGCCCTGCATCGACCTTGAAGGC 840
; Db 958 GCGTGTGCCATCTCGTTGTCAGAGCTGTGCTTGGATGATTTCTTCAAGCAGCATCATCAGGG 1197
; QY 1021 CATGAACATTCGCGAGGATTAACAGATGCTGTTTTCGGAGGCTTGAATTAACAGAT 1080
; Db 1198 TCGTGTATGCCACCGGGTCTATTGCAACTGTTTACGCGGTGATTTGAATTAACAGAT 1257
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; QY 1141 GGAACAGCTGTGCGAAGCAGACACCTGCGGTATCGGAACC 1182
; Db 1318 CGAGACCTGTGCAAAAGTACATGTCCGATACCACAC 1359

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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,526  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-201 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1617 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

US-09-363-526-1

Query Match 9.5%; Score 121.6; DB 4; Length 1617;

Best Local Similarity 49.3%; Pred. No. 1.8e-28;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

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QY 394 GGCAGTGTTCCTGGGATGCACATCAACAGATGGCTGCTTCTCATGACATTTGCCA 453
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Db 658 CTGCCAGGCTTCTGCTCTGTTGGTGAAGGACAGACAACACTCACCACGCGGCC 717

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QY 634 T-----GAGCTCACACGGCGCTCACCAGATTTCCCGCAA 666
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QY 667 GCTCATTTCAGTTCAGCAGTACTATTTCTTGGTCATCTGTATCTTGTTCGGTTCATTG 726
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Db 1078 GCAGGCGGTGTGGGAACACTGTGTGGGATCGTGTTCCTCGCTCAACGACAGGATGCC 1137

QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATCGGATTCGTTGGCCAGATCCATGAGAC 1020
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   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1258 CGAGCACCATTGTTCCTTCGATGCTTCGCCACAACTTTTCAAAGATCCAGCCTGCTGT 1317

QY 1141 GGAACAGCTGTGCCAGNAGCAGACACTGCGGTATCGGAACCC 1182
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1318 CGAGACCTGTGCAAAAAGTACAAATGTCCGATACCAACACCAC 1359
```

#### RESULT 5

US-09-330-235-17

; Sequence 17, Application US/09330235  
; Patent No. 6459018  
; GENERAL INFORMATION:  
; APPLICANT: Knutzon, Debbie  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS  
; FILE REFERENCE: MOCO.155.00US  
; CURRENT APPLICATION NUMBER: US/09/330.235  
; CURRENT FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: 60/089,043  
; PRIOR FILING DATE: 1998-06-12  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 1617  
; TYPE: DNA  
; ORGANISM: Mortierella alpina  
US-09-330-235-17

Query Match 9.5%; Score 121.6; DB 4; Length 1617;

Best Local Similarity 49.3%; Pred. No. 1.8e-28;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

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QY 394 GGCAGTGTTCCTGGGATGCACATCAACAGATGGCTGCTTCTCATGACATTTGCCA 453
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Db 538 GCGTCGCTTTTGGGTCTGTTGGCAGCAGTGGGATGTTGGCTCAGCAGCTTTTGCA 597

QY 454 CCACGAGACTTCAAGAACCGGACACTGGAACAACTCGTGGGACTGGTATTTGGCAATGG 513
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 TCACGAGGTCTTCAGGACCGTTCTGGGTGATCTTTTCGGCGCTTCTTTGGGAGGTGT 657

QY 514 TCTGCAAGGTTTTTCCGTGACATGTTGGAAGGACAGACAATGCACATCATTCGGCAAC 573
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 CTGCCAGGCTTCTGCTCTGTTGGTGAAGGACAGACAACACTCACCACGCGGCC 717

QY 574 CAATGTTCAAGGCGACGACCTGATATTGACAACTCCCGCTTAGCCTGGTCTGAGGA 633
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 718 CAACGTCCACGGGAGGATCCCGACATTCACCCACCTCTGTGACCTGGAGTGAGCA 777

QY 634 T-----GAGCTCACACGGCGCTCACCAGATTTCCCGCAA 666
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Db 778 TCGTTCGAGATGTTCTCGGATGCCAGATGAGGAGCTGACCCGCACTGTCGCGTTT 837

QY 667 GCTCATTTCAGTTCAGCAGTACTATTTCTTGGTCATCTGTATCTTGTTCGGTTCATTG 726
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 CATGGTCTGTAACGACACTGTTTACTTCCCATCTCTCGTTGCGCGCTCTCTCCTG 897

QY 727 GTGTTTCCAGTGGTGTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 898 GTCCCTCCAGTCCATTCTTGTGCTTAACGGTCAAGGACAGAGATAACCAATT 957

QY 781 CTATCGCTCTCAGTATGAAGAGGAGGACATTTGGCTCGCCCTGCACCTGGACCTTGAAGGC 840
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 958 GCAGGCGGTGTGGGAACACTGTGTGGGATCGTGTTCCTCGCTCAACGACAGGATGCC 1017

QY 841 CTGTTTCCAGTGGTGTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 900
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1018 CGCCACCATGTTCTGTTTCATCAAGGATCCCGTCAACATCTGTTGACTTTTGGTGTTC 1077

QY 901 GGAGCTGGTGGCGGCTTCGGCATTCGCATCGTGGTGTTCATGAACCACTACCCACTGGA 960
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1078 GCAGGCGGTGTGGGAACACTGTGTGGGATCGTGTTCCTCGCTCAACGACAGGATGCC 1137

QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATCGGATTCGTTGGCCAGATCCATGAGAC 1020
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1138 TGTGATCTCGAAGGAGGCGGTGCGATATGGATTTCTTCCAGGAGGACATCATCAGGG 1197
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Qy	901	GGAGCTCGTGTGGGGCTTCGGCATTCGGATCGGTGTTTCATGAACACATACCACACTGGA	960
Db	1078	GCAGGGCGGTGCGGAAACTTGTGGCGATCGTGTTCCTCGCTCAACCAACAGTATGCC	1137
Qy	961	GAAGATCGGGGACCCAGTCTGGGATGCCATGATTCCTCGGTTGGCCAGATCATGAGAC	1020
Db	1138	TGTGATCTCGAAGGAGGAGCGGTGCGATATGGATTCTTCACGACGAGATCATACGGG	1197
Qy	1021	CATGACATCTGGGAGGAGATATACAGATATGGTTTTTCGGAGCGTTGAATTACCAGAT	1080
Db	1198	TCGTGATGTCCACCCGGGTCTATTGGCCAACTCGGTTCAACGGGTGGATTGAATCATCAGAT	1257
Qy	1081	TGAGCACCATTTGTGGCCGACCTCCCTCGCCACAACTCAGACGGGTAGCTACCAGGT	1140
Db	1258	CGAGCACCATTTGTTCCCTTCGATGCTCGCCACAACTTTTCAAAGATCCAGCGCTGCTGT	1317
Qy	1141	GGAAACAGCTGTGCAGAGCACAACTGCGGTATCGGAACCC	1182
Db	1318	CGAGACCCCTGTGCAAAAGTACAATGTCCCGATACCAACACCAC	1359

## RESULT 6

US-08-831-570-1  
; Sequence 1, Application US/08831570

## : GENERAL INFORMATION:

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;
; ADDRESS: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
;
```

REF. 11330  
COMPUTER READABLE FORM.

?  
? COUNTRY READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? COMPUTER: IBM PC compatible  
? OPERATING SYSTEM: PC-DOS/MS-DOS  
? SOFTWARE: PatentIn Release #1.0, Version #1.30  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: US/08/831,570  
? FILING DATE: 09-APR-1997  
?

/ CLASSIFICATION: /  
 / ATTORNEY/AGENT INFORMATION: /  
 / NAME: DIGiglio, Frank S. /  
 / REGISTRATION NUMBER: 31,346 /  
 / REFERENCE/DOCKET NUMBER: 10545 /  
 / TELECOMMUNICATION INFORMATION: /  
 / TELEPHONE: (516) 742-4343 /  
 / TELEFAX: (516) 743-4366 /  
 / INFORMATION FOR SEQ ID NO: 1: /

```

, , , SEQUENCE CHARACTERISTICS:
, , , LENGTH: 1694 base pairs
, , , TYPE: nucleic acid
, , , STRANDEDNESS: double
, , , TOPOLOGY: linear
, , , MOLECULE TYPE: DNA (genomic)
, , , FEATURE:
, , , NAME/KEY: CDS
, , , LOCATION: 43..1387
, , , US-08-831-570-1

```

Query Match	4.1%	Score 51.8;	DB 2;	Length 1684;
Best Local Similarity	56.9%	Pred. No. 3e-06;		

QY 1007 CAGATCCATGAGACCATGAACATTCGGCGAGGGATTATCACAGATTGGTTTTTCGGAGGC 1066

[illegible]

## RESULT. T 7

RES001 /  
US-08-831-575-1  
; Sequence 1, Application US/08831575

## ; Patent No. 5977436

```

: GENERAL INFORMATION:
:
: APPLICANT: Thomas, Terry L.
:
: APPLICANT: Li, Zhongsen
:
: TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
:
: TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
:
: NUMBER OF SEQUENCES: 33
:
: CORRESPONDENCE ADDRESS:
:

```

```

; ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER
;
; STREET: 400 Garden City Plaza
;
; CITY: Garden City
;
; STATE: New York
;
; COUNTRY: U.S.A.
;
; ZIP: 11530
;

```

REF: T1000  
COMPUTER READABLE FORM:

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?  
?      CURRENT APPLICATION DATA:  
?      SOFTWARE: PatentIn Release #1.0, Version #1.30  
?      OPERATING SYSTEM: PC-DOS/MS-DOS  
?      COMPUTER: IBM PC compatible  
?      MEDIUM TYPE: Floppy disk  
?      INSTRUCTIONS FOR USER:  
?      COMMENTS:
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```

: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: DIGiglio, Frank S.
: REGISTRATION NUMBER: 31,346
: REFERENCE/DOCKET NUMBER: 10203
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (516) 742-4343
: TELEFAX: (516) 742-4366
:

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Best Local Similarity	56.9%	Pred. No. 3e-06;		

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Dδ		1090	CAAACGGATGGGACACTTGACATTTCTGTCTCCTTGGATGGATTGGTTTTCATGTGTGA	1149

QY 1067 TTGAATTACGAGATTGAGACCATTTGTGGCGACCCCTCCCTCGCCACACCTGACAGCG 1126

Qy	— — — — — — — — — — — — — — —	1127 GTTAGCTACCAAGGTGGAACAGCTGTGCCAGAAGCACAACCTGCCGTA 1173
Db	— — — — — — — — — — — — — — —	1210 ATCTCGCCCTACGTGATCGAGTTATGCAAGAAACATAATTGGCCTTA 1256



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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,254  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 838321XWVU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1685 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-934-254-4

Query Match 4.1%; Score 51.8; DB 4; Length 1685;  
Best Local Similarity 56.9%; Pred. No. 3e-06;  
Matches 95; Conservative 0; Mismatches 72; Indels 0; Gaps 0;  
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DB 1091 CAACCGATGGGACACTTGACATTTCTGTCTCTCTGGATGGATTGTTTCATGGTGA 1150  
QY 1067 TTGAATACAGATTGAGCACCATTGTGGCGGACCTCCCTGCCACACAACTGACAGCG 1126  
DB 1151 TTGCAATTCGAATGAGCATCTTGTTCCTCCCAAGATGCTAGATGCAACCTTAGGAAA 1210  
QY 1127 GTTAGTACAGGTGGACAGCTGTGCCAGAACGACAACTGCGCGTA 1173  
DB 1211 ATCTCGCCTACGTGATCGAGTTATGCAAGAAACATAATTGGCTTA 1257

RESULT 11  
US-09-439-261-6  
; Sequence 6, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P2  
; CURRENT APPLICATION NUMBER: US/09/439,261  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1686  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-439-261-6

Query Match 4.0%; Score 51; DB 4; Length 1686;  
Best Local Similarity 46.7%; Pred. No. 5.4e-06;  
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGAGGCCATTGGCCTCGCCCTGCACCTGGACCTTGAAGGCCCTGTTCAC 850  
DB 261 CATAAGAACTGGGTGGACCTGGCCTGGGCCGTAGCTACTACATCCGGTTCTTCATCACC 320  
QY 851 TTATTCTTTATGCCAGCATCCTCACATCGCTGTGGTGTGTTTTCGTTTCGGAGCTGGTT 910  
DB 321 TACATCCCTTTCTAGGGCATCTCGGAGCCCTCTCTTTCCTCAACTTCATCAGGTTCTCG 380  
QY 911 GCGGCTTCGGCATTCGGATCGTGTTCATGAACCACTACCCCACTGGAGAGATCGGG 970  
DB 381 GAGAGCCACTGGTTTGTGGGTACACAGATGAATCATCATCGTTCATGAGATTGACCCAG 440  
QY 971 GACCCAGTCTGGGATGCCCATGGATTCTCGGTTGGCCAGATCCATGAGACCATGAACATT 1030  
DB 441 GA-----GGCCTACCGTACTGGTTCAGTACGAGCTGACAGCCACCTGCAACGCTG 491  
QY 1031 CCGGAGGGATTATCACAGATTGTTTTCGGAGGCTTGAATTACCACTTCAGCACTTCAGCACCATT 1090  
DB 492 GAGCAGTCTTCTTCAAGCACTGGTTCAGTGGACACCTTAATCTCCAGATTGAGCACCAC 551  
QY 1091 TTGTGGCGGACCTCTCTCGCCACAACTGACAGCGTTAGCTACCAAGTGGAGACAGCTG 1150  
DB 552 CTCTTCCCACTGCGCCGACAACTTACACAAAGATCGCCCGCTGGTGAAGTCTCTA 611  
QY 1151 TGCAGAGACACAACTGCGCTATCGGNAACCGCTGCCCATGAAGGTTGGTCACTCCTG 1210  
DB 612 TGTGCCAAGCATGTCATTGAATACAGGAGAGCGCTACTGAGGCGCTCTGCTGGACATC 671  
QY 1211 CTGGCTATCTGGCGGTGT 1229  
DB 672 ATCAGGTCCTCGAAGAACT 690

RESULT 12  
US-09-227-613-6  
; Sequence 6, Application US/09227613A  
; Patent No. 6432684  
; GENERAL INFORMATION:  
; APPLICANT: MUKERJI, Pardip  
; APPLICANT: LEONARD, Amanda E.  
; APPLICANT: HUANG, Yung-Sheng  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.P1  
; CURRENT APPLICATION NUMBER: US/09/227,613A  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
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; SEQ ID NO 6  
; LENGTH: 1686  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-227-613-6

Query Match 4.0%; Score 51; DB 4; Length 1686;  
Best Local Similarity 46.7%; Pred. No. 5.4e-06;  
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGAGGCCATTGGCCTCGCCCTGCACCTGGACCTTGAAGGCCCTGTTCAC 850  
DB 261 CATAAGAACTGGGTGGACCTGGCCTGGGCCGTAGCTACTACATCCGGTTCTTCATCACC 320  
QY 851 TTATTCTTTATGCCAGCATCCTCACATCGCTGTGGTGTGTTTTCGTTTCGGAGCTGGTT 910  
DB 321 TACATCCCTTTCTAGGGCATCTCGGAGCCCTCTCTTTCCTCAACTTCATCAGGTTCTCG 380  
QY 911 GCGGCTTCGGCATTCGGATCGTGTTCATGAACCACTACCCCACTGGAGAGATCGGG 970  
DB 381 GAGAGCCACTGGTTTGTGGGTACACAGATGAATCATCATCGTTCATGAGATTGACCCAG 440  
QY 971 GACCCAGTCTGGGATGCCCATGGATTCTCGGTTGGCCAGATCCATGAGACCATGAACATT 1030

Db 441 GA-----GGCCTACCGTGACTGGTTTCAGTAGCCACTGACACCCACTGCTCAAGCTG 491  
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QY 1211 CTGCGCTATCTGGCGGTGT 1229  
Db 672 ATCAGGTCCCTGAAGAAGT 690

## RESULT 13

US-09-439-261-7

; Sequence 7, Application US/09439261

; Patent No. 6428990

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pradiip

; APPLICANT: Leonard, Amanda E.

; APPLICANT: Huang, Yung-Sheng

; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

; FILE REFERENCE: 6295.US.P2

; CURRENT APPLICATION NUMBER: US/09/439,261

; CURRENT FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: US 08/833,610

; PRIOR FILING DATE: 1997-04-11

; PRIOR APPLICATION NUMBER: PCT/JUS98/07422

; PRIOR FILING DATE: 1998-04-10

; PRIOR APPLICATION NUMBER: US 09/227,613

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-439-261-7

Query Match 4.0%; Score 51; DB 4; Length 1843;

Best Local Similarity 46.7%; Pred. No. 5.7e-06;

Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGCCATTTGGCTCGCCCTGCACTGGACCTTGAAGGCCCTGTTCCAC 850  
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QY 851 TTATTTCTTTATGCCAGCATCTACATCGCTGTTGGTGTTCCTTTCGGAGCTGGT 910  
Db 478 TACATCCCTTTACGGCATCTCTGAGGCCCTCCCTTTCTCAACTTCATCAGGTTCC 537  
QY 911 GCGCGGTTCGGCATTCGGATCGTGTGTTTCATCAACCACTACCCATCGGAGAGATCG 970  
Db 538 GAGAGCACTGGTTGTGGTGCACACAGATGAATCAGATCGTCATGAGATTGAC 597  
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QY 1211 CTGCGCTATCTGGCGGTGT 1229  
Db 829 ATCAGGTCCCTGAAGAAGT 847

## RESULT 15

US-09-439-261-8

; Sequence 8, Application US/09439261

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QY 1151 TCCCAAGACCAACCTGCGGTATCGGAACCCGCTGCCCATGAAGGTTGGTCATCTG 1210  
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QY 1211 CTGCGCTATCTGGCGGTGT 1229  
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## RESULT 14

US-09-227-613-7

; Sequence 7, Application US/09227613A

; Patent No. 6432684

; GENERAL INFORMATION:

; APPLICANT: MUKERJI, Pradiip

; APPLICANT: LEONARD, Amanda E.

; APPLICANT: HUANG, Yung-Sheng

; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

; FILE REFERENCE: 6295.US.P1

; CURRENT APPLICATION NUMBER: US/09/227,613A

; CURRENT FILING DATE: 1999-01-08

; PRIOR APPLICATION NUMBER: 08/833,610

; PRIOR FILING DATE: 1997-04-11

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-227-613-7

Query Match

Best Local Similarity 46.7%; Pred. No. 5.7e-06;

Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGCCATTTGGCTCGCCCTGCACTGGACCTTGAAGGCCCTGTTCCAC 850  
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QY 851 TTATTTCTTTATGCCAGCATCTACATCGCTGTTGGTGTTCCTTTCGGAGCTGGT 910  
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QY 1091 TTGTGGCCGACCTCCCTCGCCACACCTGACAGGGTTAGTACCAGGTGGAACAGCTG 1150  
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QY 1211 CTGCGCTATCTGGCGGTGT 1229  
Db 829 ATCAGGTCCCTGAAGAAGT 847

## RESULT 15

US-09-439-261-8

; Sequence 8, Application US/09439261



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Job time : 76.7752 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
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9184.672 Million cell updates/sec

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Perfect score: 1275  
Sequence: 1 atttttttcgaatgaagt.....gcggggaagctctataagg 1275

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	56	4.4	657	10	US-09-770-149-494
4	56	4.4	1350	9	US-09-938-842A-558
5	51.8	4.1	1685	12	US-10-029-756-4
6	51	4.0	1474	9	US-10-102-806-232
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9	51	4.0	2257	9	US-10-191-513A-8
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18	47.6	3.7	1702	12	US-10-029-756-26
19	45.6	3.6	473	9	US-10-191-513A-36

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21	45.2	3.5	1478	9	US-09-981-876-63	Sequence 63, Appl
22	45.2	3.5	1478	9	US-09-148-545-63	Sequence 63, Appl
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25	44.8	3.5	960	9	US-10-191-513A-35	Sequence 35, Appli
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27	44.2	3.5	2016	9	US-09-981-876-119	Sequence 119, App
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30	43.4	3.4	347	9	US-09-902-941-355	Sequence 355, App
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32	43.4	3.4	347	9	US-09-849-626-355	Sequence 355, App
33	43.4	3.4	347	9	US-10-017-754-355	Sequence 355, App
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36	41	3.2	6344	9	US-10-209-776-1	Sequence 1, Appli
37	38.4	3.0	1479	9	US-10-156-761-1811	Sequence 1, Appli
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43	35.6	2.8	533	9	US-10-184-644-44	Sequence 44, Appl
44	35.6	2.8	533	9	US-10-184-644-44	Sequence 44, Appl
45	35	2.7	428	10	US-09-876-889-246	Sequence 246, App

ALIGNMENTS

RESULT 1

US-09-967-477B-7  
; Sequence 7, Application US/09967477B  
; Patent No. US20020156254A1  
; GENERAL INFORMATION:  
; APPLICANT: Xiao Qiu  
; APPLICANT: Haiping Hong  
; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL  
; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: BNZ-001  
; CURRENT APPLICATION NUMBER: US/09/967,477B  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/236,303  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/297,562  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1380  
; TYPE: DNA  
; ORGANISM: Thraustochytrium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1380)  
US-09-967-477B-7

Query Match

Best Local Similarity	8.4%	Score 107.4;	DB 9;	Length 1380;
Matches 484;	Conservative 0;	Mismatches 491;	Indels 42;	Gaps 4;
QY	251	TTCCGGAAGCTCCGAGAAGAGTTGATCGCAACTGGCATGTTGATGCTCCCTCCCTCTGG	310	
Db	334	TACCGTCGTCGCGGCTCAAGGTCAGGTCATGGGCTCTACACGCCACCGCGCTCTAC	393	
QY	311	TACTCATACAAATCAGCAC	361	
Db	394	TACGCGTGAAGCTCGTGAGCAGCTTCGCGCATCGCGTCTCTCGATGGCGATCTGCTTC	453	
QY	362	CTGATGGTTCAGTATCAGATGATTTTCATTTGGGCGAGTGTGCTTGGGATGCATCAAA	421	
Db	454	TTCTTCAACAGTTTCTGCCCATGATGATGGTGGCGGCTGATTTATGGGGCTCTTCTACCAG	513	

```
QY 422 CAGATGGCGTGGCTTCTCATGACATTTGCACACACAGACTTTCAAGAACCGAACTGG 481
DB 514 CAGTCGGATGGCTGGCGCAGACTTCTTGCACAAACAGAGTGTGCGAGAACCGCACGCTC 573
QY 482 AACAAACCTCGTGGAGCTGATTTTGGCAATGGTCTGCAAGGTTTTCGGTGACATGTTGG 541
DB 574 GGCAACCTTATCGGCTCGCTCGTGGGCAACGCTGGCAGGCTTCAGCGTGCAGTGGTG 633
QY 542 AAGCAGACAGACATGTCGACATCATTCGGCAACCAATGTTCAAGG-----585
DB 634 AAGAACAAGCACAACCTGCAACCGCGGTGCGCAACCTGCACAGCGCAAGAGGAGGCG 693
QY 586 -----GCACGACCTGATATTGACAACCTCCGCCCTTAGCTGTGAGGATGAGTGC 640
DB 694 TTATCGGCGCGGAGATCGACACCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
QY 641 ACACGGGC-----GTCCAGGATTTCCCGAAGCTCATTCAGTTCCAGCAGTACTATTTC 694
DB 754 CGCAAGCGGTTGAGTTCGGCGCAGCGCGCTTCTTCATCCGCAACGAGCGTTCCTATAC 813
QY 695 TTGGTCATCTGATCTGTTGGGTTCATTTGGTGTGTTCCAGTGTGTTGACGTCGCG 754
DB 814 TTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873
QY 755 AGTTTGAAGCAGACAGATACCAATTTCTATCGCTCTCAGTATATAAGAGGAGGCCATGGC 814
DB 874 ACCGAGTTCGTTCCGCTATCTTCGACAAAGTGTGAGTTCGACGAGCGGAGAGCGGGT 933
QY 815 CTCGCCCTCGACCTGGACCTTGAAGCGCTGTTCCACTTATTTTATGCCAGCATCTC 874
DB 934 CTGATCGTGCATACATCTGCGAGCTCGCGATCCGCTACTTCTCAACATGAGCTGTT 993
QY 875 ACATCGCTGTTGTTGTTTTCGTTTCGAGCTGTTGCGGCTTCGCGCATGCGATCGT 934
DB 994 GAGGGGCTGCGCATCTTCTCATGTCGCGCAGCGCTCTGCGGCTTGTCTGCGCTGGT 1053
QY 935 GTGTTTCATGAACCACTACCCACTGGAGAAGATCGGACCCAGCTCTGGATGGCATGGA 994
DB 1054 TTCAGTATGGCCACACGCGATGCTGGTGTACGAGCGCGAACCAG-----CCGAC 1107
QY 995 TTCTCGGTTGGCAGATCCATGAGACCATGAACATTCGGCAGGGGATTATCACAGATTGG 1054
DB 1108 TTCTGCGAGCTGAGGTGACACGACGCGCAACATCGCGCTGCGTATTCATGAGCTGG 1167
QY 1055 TTTTTCGAGGCTTGAATACCAATGAGACCATTTGTGGCGGACCTCCCTCGGCAC 1114
DB 1168 TTCACGGGTGGCTTGAATACCAATGAGACCATACCTGTTCGCGCTGTCGCGCGCAC 1227
QY 1115 AACCTGACAGCGGTAGCTACCAAGTGGAAAGATGTCGAGAGCAGCAACCTGCGCTAT 1174
DB 1228 AACTGCGCAAGGTCAAGCTGCTCATCAAGTGTATGCAAGAGTTCGACATCCCGTTC 1287
QY 1175 CGGAACCGCTGCCCCATGAAGGTGGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
DB 1288 CACGAGACCGGCTTCTGGGAGGCGATCTACGAGTCTGTGACCAACCTGCGGAGCATC 1344
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## RESULT 2

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US-09-924-035A-370/c
; Sequence 370, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Grlach, Jn
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSEQ for Windows Version 3.0
```

```
; SEQ ID NO 370
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-924-035A-370

Query Match 4.4%; Score 56; DB 10; Length 480;
Best Local Similarity 60.5%; Pred. No. 5,1e-08;
Matches 92; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1045 CACAGATTGGTTTTCGGAGGCTTGAATTACCAAGTTCGACCATTTTGGCCGACCT 1104
DB 456 CATGATTGGTTCTTTGGTGTATACAGTTTCAGCTTGAGCATCATTTTCCCTCGCTT 397
QY 1105 CCCTCGCCCAACCTGACAGCGGTAGTACCAAGTTCGACCATTTTGGCCGACCA 1164
DB 396 ACCTCGTTCGATCTCCGAAAGTTTCTCCGGTGTTCAGAGCTTTCGAAGAGCATAA 337
QY 1165 CTTGCCGTATCGGAACCGCTGCCCATGAAG 1196
DB 336 TCTCCGTATAGGATGATGCTGTTGAAG 305
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## RESULT 3

```
US-09-770-149-494/c
; Sequence 494, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Grlach, Jn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 494
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-494
```

```
Query Match 4.4%; Score 56; DB 10; Length 657;
Best Local Similarity 60.5%; Pred. No. 6.3e-08;
Matches 92; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1045 CACAGATTGGTTTTCGGAGGCTTGAATTACCAAGTTCGACCATTTTGGCCGACCT 1104
DB 413 CATGATTGGTTCTTTGGTGTATACAGTTTCAGCTTGAGCATCATTTTCCCTCGCTT 354
QY 1105 CCCTCGCCCAACCTGACAGCGGTAGTACCAAGTTCGACCATTTTGGCCGACCA 1164
DB 353 ACCTCGTTCGATCTCCGAAAGTTTCTCCGGTGTTCAGAGCTTTCGAAGAGCATAA 294
```



```
Query Match 4.0%; Score 51; DB 9; Length 1474;
Best Local Similarity 46.7%; Pred. No. 5.1e-06;
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGAGCCATTGGCCCTCGCCCTCACTGGACCTTGAAAGCCCTGTTCAC 850
DB 396 CATAAGAACTGGGTGACCTGGCCCTGGCGCTCAGTACTACATCCGGTTCCTCATCACC 455
QY 851 TTATTTCTTTATGCCAGCATCTCTCATCGCTGTGTGGTGTTCGTTTCGGAGCTGGT 910
DB 456 TACATCCCTTTCTACGGCATCTCTGGAGCCCTCTTTTCTCACTCACTCAGTTCTG 515
QY 911 GCGGGCTTGGCATTCGGATCGTGTGTTCATGAACCACTACCCACTGAGAGATCGGG 970
DB 516 GAGAGCACTGGTGTGTGGGTCACACAGATGAATCAGATCTGTATGAGATTTGACCA 575
QY 971 GACCCAGTCTGGGATGGCCATGCTGCTGTGGTGGCCAGATCCATGAGACCATGAACAT 1030
DB 576 GA-----GSCCTACCTGACTGTTTCAGTAGCAGCTGACAGCCACTTCAACGTG 626
QY 1031 CGCGAGGATTTATCAGATTCCTGCTGTGTGGTGTTCGTTTCGGAGCTGGT 1090
DB 627 GAGCAGTCTCTTCAACGACTGTTTCAGTGGACACCTTAACCTCCAGATTTGAGACCA 686
QY 1091 TTGTGCGGACCTCTCTCGCCCAACCTGACAGCGTTAGCTTACAGGTGGAACAGCTG 1150
DB 687 CTCCTCCCACTGCTGCTGCGGCAACCTTACACAAGATGCCCGCTGGTGAAGTCTCTA 746
QY 1151 TGCAGAAGCACAACTGCGGTATCGGAACCCCTGCCCCATGAAGGTTGGTCACTCTG 1210
DB 747 TGTGCCAAGCATGGCATTTGATACAGGAGAACCGCTACTGAGGCCCTGCTGGACATC 806
QY 1211 CTGCGTATCTGCGGTGT 1229
DB 807 ATCAGGTCCCTGAAGAAGT 825

RESULT 7
US-10-191-513A-6
; Sequence 6, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-6

Query Match 4.0%; Score 51; DB 9; Length 1686;
Best Local Similarity 46.7%; Pred. No. 5.6e-06;
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGAGCCATTGGCCCTCGCCCTGACCTGGACCTTGAAAGCCCTGTTCAC 850
DB 261 CATAAGAACTGGGTGACCTGGCCCTGGCGCTCAGTACTACATCCCGTTCCTCATCACC 320

Query Match 4.0%; Score 51; DB 9; Length 1686;
Best Local Similarity 46.7%; Pred. No. 5.6e-06;
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGAGCCATTGGCCCTCGCCCTGACCTGGACCTTGAAAGCCCTGTTCAC 850
DB 261 CATAAGAACTGGGTGACCTGGCCCTGGCGCTCAGTACTACATCCCGTTCCTCATCACC 320
```

```
QY 851 TTATTTCTTTATGCCAGCATCTCTCATCGCTGTGTGGTGTTCGTTTCGGAGCTGGT 910
DB 321 TACATCCCTTTCTACGGCATCTCTGGAGCCCTCTTTTCTCACTTCACTCAGTTCTCTG 380
QY 911 GCGGGCTTGGCATTCGGATCGTGTGTTCATGAACCACTACCCACTTGGAGATCGGG 970
DB 381 GAGAGCACTGGTGTGTGGGTCACACAGATGAATCAGATCTGTATGAGATTTGACCA 440
QY 971 GACCCAGTCTGGGATGGCCATGATTCCTGCGTGGCCAGATTCATGAGACCATGAACAT 1030
DB 441 GA-----GSCCTACCTGACTGTTTCAGTAGCAGCTGACAGCCACTTCAACGTG 491
QY 1031 CGCGAGGATTTATCAGATTCCTGCTGTGTGGTGTTCGTTTCGGAGCTGGT 1090
DB 492 GAGCAGTCTCTTCAACGACTGTTTCAGTGGACACCTTAACCTCCAGATTTGAGACCA 551
QY 1091 TTGTGCGGACCTCTCTCGCCCAACCTGACAGCGTTAGCTTACAGGTGGAACAGCTG 1150
DB 552 CTCCTCCCACTGCTGCTGCGGCAACCTTACACAAGATGCCCGCTGGTGAAGTCTCTA 611
QY 1151 TGCAGAAGCACAACTGCGGTATCGGAACCCCTGCCCCATGAAGGTTGGTCACTCTG 1210
DB 612 TGTGCCAAGCATGGCATTTGAATACAGGAGAACCGCTACTGAGGCCCTGCTGGACATC 671
QY 1211 CTGCGTATCTGCGGTGT 1229
DB 672 ATCAGGTCCCTGAAGAAGT 690

RESULT 8
US-10-191-513A-7
; Sequence 7, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-513A-7

Query Match 4.0%; Score 51; DB 9; Length 1843;
Best Local Similarity 46.7%; Pred. No. 6e-06;
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGAGCCATTGGCCCTGCGCTGACCTGGACCTTGAAAGCCCTGTTCAC 850
DB 418 CATAAGAACTGGGTGACCTGGCCCTGGCGCTCAGTACTACATCCCGTTCCTCATCACC 477
QY 851 TTATTTCTTTATGCCAGCATCTCTCATCGCTGTGTGGTGTTCGTTTCGGAGCTGGT 910
DB 478 TACATCCCTTTCTACGGCATCTCTGGAGCCCTCTTTTCTCACTTCACTCAGTTCTCTG 537
QY 911 GCGGGCTTGGCATTCGGATCGTGTGTTCATGAACCACTACCCACTTGGAGATCGGG 970
DB 538 GAGAGCACTGGTGTGTGGGTCACACAGATGAATCAGATCTGCTGAGATTTGACCA 597
```

QY 971 GACCCAGTCTGGGATGCCATGATTCCTCGTTGGCCAGATCCATGAGACCATTGAACATT 1030  
DB 598 GA-----GCGCTACCGTGACTGGTTCAAGTAGCCAGCTGACAGCCACCTGCAAGTG 648  
QY 1031 CGCGGAGGATATACAGATTGGTTTTCGGAGGCTTGAATTACAGATTGAGCACCAT 1090  
DB 649 GAGCAGTCTCTTCAACGACTGGTTTCAGTGGACACTTAACCTCCAGATTGAGCACCAC 708  
QY 1091 TTGTGGCCGACCTCCCTCCGCNACAACTGACAGCGGTAGCTTACAGGTGGAGACAGCTG 1150  
DB 709 CTCCTTCCCACTGCGCCGACAACTTACACAAGATGCCCGCTGGTGAAGTCTCTA 768  
QY 1151 TGCCAGAACCAACCTGCGGTATCGGAACCCGCTGCCCATGAAGGTTGGTCATCCTG 1210  
DB 769 TGTGCCAACATGGCATTTGAATCCAGGAGAGCCGCTACTGAGGCGCCCTGCTGGACATC 828  
QY 1211 CTGCGCTATCTGCGGTGT 1229  
DB 829 ATCAGGTCCCTGAAGAAGT 847

## RESULT 9

US-10-191-513A-8  
; Sequence 8, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Dag  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; PRIOR FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 2257  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-191-513A-8

Query Match 4.0%; Score 51; DB 9; Length 2257;  
Best Local Similarity 46.7%; Pred. No. 6.8e-06;  
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAGAGGAGGCCATGGCCCTCGCCCTGCACTGGACCTTGAGGCCCTGTTCAC 850  
DB 832 CATAGAACTGGTGGAGCTGGCCCTGGCCGCTGAGCTACTATACATCGGTTCTTCATCACC 891  
QY 851 TTATTTCTTATGCCAGCATCTCATCGCTGTTGGTGTCTTTTCGTTTCGGAGCTGGTT 910  
DB 892 TACATCCCTTTCTACGGGATCTCTGGAGCCCTCTTTCTCACTTCATCAGGTTCTGT 951  
QY 911 GCGGCTTCGGCATTCGTGTTGTCATGAACCACTACCCACTGGAGAGATCGGG 970  
DB 952 GAGAGCCACTGGTTGTGGTGCACACAGATGAATACATCGTCATGGAGATTGACCCAG 1011  
QY 971 GACCCAGTCTGGATGGCCATGGATTCTCGGTGGCCAGATCCATGACACATGAACATT 1030  
DB 1012 GA-----GGCCTACCGTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACGCTG 1062  
QY 1031 CGCGGAGGATTATACAGATTGGTTTTCGGAGGCTTGAATTACAGATTGAGCACCAT 1090  
DB 1063 GAGCAGTCTTCTTCAACGACTGGTTTCAAGTGACACCTTAACCTCCAGATTGAGCACCAC 1122

QY 1091 TTGTGGCGGACCTCCCTCGCCACAACCTGACAGCGGTAGCTACCAAGTGGAAACAGCTG 1150  
DB 1123 CTCTTCCCACTGCGCCGCAACAACCTTACACAAGATCGCCCGCTGGTGAAGTCTCTA 1182  
QY 1151 TGCCAGAACCAACCTGCGGTATCGGAACCCGCTGCCCATGAAGGTTGGTCATCCTG 1210  
DB 1183 TGTGCCAAGCATGGCATTTGAATCCAGGAGAGCGGCTACTGAGGGGCCCTGCTGGACATC 1242  
QY 1211 CTGCGCTATCTGCGGTGT 1229  
DB 1243 ATCAGGTCCCTGAAGAAGT 1261

## RESULT 10

US-10-156-761-1580  
; Sequence 1580, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 1580  
; LENGTH: 1059  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1059)  
US-10-156-761-1580

Query Match 3.9%; Score 49.6; DB 9; Length 1059;  
Best Local Similarity 56.9%; Pred. No. 1.2e-05;  
Matches 91; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 961 GAAGATCGGGGACCCAGTCTGGGATGGCCATGATTCGTTGGCCAGATCCATGAGAC 1020  
DB 762 GGAATATGCGCGACCCGAGCCACACGCTTGGGCCACTCGCGCGACAGGTCCTCACCTC 821  
QY 1021 CATGACATTCGCGAGGGGATTATCACAGATTGGTTTTCGGAGGCTTGAATTACCAGAT 1080  
DB 822 GGCACAGCTGGCGGGGCGTCCGCTGACCGAGTGGTCTCGGGGACTCAACTACCAGAT 881  
QY 1081 TGAGCACCATTTTGTGCGCGACCTCCCTCGCCACAACCTG 1120  
DB 882 CGAGCACCATCTGTTCCCGAGCATGCCCGCCCCCACTTG 921

## RESULT 11

US-10-156-761-1/C  
; Sequence 1, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRO

```
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      3.8%; Score 49.6; DB 9; Length 9025608;
Best Local Similarity 56.9%; Pred. No. 0.0045;
Matches 91; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 961 GAAGATCGGGGACCCAGTCTGGGATGGCCATGGATTCTCGGTGGCCAGATCCATGAGAC 1020
Db 1953719 GGAATGCCGACCCGACGACACACGCTTGGGCCACCTGGCGGACAGGTCTCACCTC 1953660

Qy 1021 CATGAACATTCGGGAGGAGGATATACAGATTTGTTTCGGAGGCTTGAATTACCAGAT 1080
Db 1953659 CGCAACATTCGGGCGGCTCGGCTGACGAGTGTCTCGCGGAGTCAACTACCAGAT 1953600

Qy 1081 TGACACATTTGTGGCGGACCCCTCCCTCGGCACACACCTG 1120
Db 1953599 CGAGCACCATCTGTTCCGAGCATGCCCGCCGCCACCTTG 1953560
```

```
RESULT 12
US-10-156-761-2285
; Sequence 2285, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2285
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1095)
US-10-156-761-2285

Query Match      3.8%; Score 48.6; DB 9; Length 1095;
Best Local Similarity 51.6%; Pred. No. 2.7e-05;
Matches 111; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 961 GAAGATCGGGGACCCAGTCTGGGATGGCCATGGATTCTCGGTGGCCAGATCCATGAGAC 1020
Db 762 GGAGTTCGGCGGACGAGGAGACCCCTGGATGGCTGGGAGCGGAGGCTCTCACCTC 821
```

```
Qy 1021 CATGAACATTCGGGAGGAGGATATACAGATTTGTTTCGGAGGCTTGAATTACCAGAT 1080
Db 822 CGGCAACATCCGCCCTCCCTGTTTCATCGACTTCTCTAGCGGCGCTCAACTACCAGT 881

Qy 1081 TGAGCACCATTTGTGGCGGACCCCTCCCTCGGCACACACCTTGACAGCGGTTAGCTACCAGT 1140
Db 882 CGAGCACCACTCTTCCCGGCTATGCCAGAGAACTTGGCGGCGCGCTGAACCTCAC 941

Qy 1141 GGAACAGCTGTGCCAGAGCACAACTCGCGGTATC 1175
Db 942 CCGCGCTACTGCGCGAGCGCGGTGTGCGGTATC 976
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RESULT 13
US-10-191-513A-37
; Sequence 37, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295, US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: k = g or t/u at position 5
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)...(6)
; OTHER INFORMATION: m = a or c at position 6
US-10-191-513A-37
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Best Local Similarity 50.4%; Pred. No. 1.8e-05;
Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 1006 CCAGATCCATGAGACCATGACATTCGGCGGAGGATTATCAGAGTTGTTTTCGGAGG 1085
Db 181 CCAGCTCCAGGCCACATGCAATGTCCCAAGTCTGCTTCAATGACTGTTTCAGTGACA 240

Qy 1066 CTTGAATTACAGATTGACACACATTTGTGGCGGACCCCTCCCTCGGCACAACTTGACAGC 1125
Db 241 CCTCAACTTCCAGATTGAGCACCATCTTTTCCACAGATGCTTCCAGACAAATTAACCAAA 300

Qy 1126 GGTTAGCTACAGGTGGAAACAGCTGTGCGCAGAGCAACACCTCCGCTATCGGAACCGCT 1185
Db 301 AGTGGTCCCTCGGTGTCAGTCTCTTGTGTGCCAGCATGGCATAGATACCAAGTCCCAAGCC 360

Qy 1186 GCCCATGAGGTTGGTCTATCTGCTATCTGCGGTGTTTCGCCGGAT 1239
Db 361 CCTGTGTGAGCCTTCGCCGACATCATCTCACTAAAGAGTACAGGCGAGCT 414
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RESULT 14
US-10-191-513A-3
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Sequence 3, Application US/10191513A  
Publication No. US20030104596A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pardip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Tapas, Das  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF.  
FILE REFERENCE: 6295.US.D3  
CURRENT APPLICATION NUMBER: US/10/191,513A  
CURRENT FILING DATE: 2002-09-25  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 655  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-191-513A-3

Query Match 3.8%; Score 48.4; DB 9; Length 655;  
Best Local Similarity 50.4%; Pred. No. 2.3e-05;  
Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;  
QY 1006 CCAGATCCATGAGACCATGACCAATTCGGCGAGGATTATCACAGATTGTTTTTCGGAGG 1065  
DB 175 CCAGCTCCAGGCCACATGCAATGTCACAAGTCTGCCTTCAATGACTGTTTCAGTGGACA 234  
QY 1066 CTTGAATTACCAAGATTGACACCATTTGTGGCGACCCCTCCCTCGCCACAACCTGACAGC 1125  
DB 235 CCTCAACTCCAGATTGACACCATCTTTTCCACAGATGCTTCCACAGATGCTTCCACAA 294  
QY 1126 GGTAGTACCAGGTGGACAGCTGTGCGCAGAGCAACCTGCCGTATCGGAAACCCGCT 1185  
DB 295 AGTGCTCCCTCCCTGGTGCAGTCTTGTGTCACAGATGTCATAGATGACAGTCCCAAGCC 354  
QY 1186 GCGCATGAAGGTTGGTGCATCTGCTGCGCTATCTGCGGGTGTTCGCCCGGAT 1239  
DB 355 CTTGCTGTCAGCCTTCGCCGACATCATCCACTCACTAAAGGAGTCCAGGGCAGCT 408

RESULT 15  
US-10-191-513A-13  
Sequence 13, Application US/10191513A  
Publication No. US20030104596A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pardip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Tapas, Das  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.D3  
CURRENT APPLICATION NUMBER: US/10/191,513A  
CURRENT FILING DATE: 2002-09-25  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 864  
TYPE: DNA  
ORGANISM: Homo sapiens

US-10-191-513A-13  
Query Match 3.8%; Score 48.4; DB 9; Length 864;  
Best Local Similarity 50.4%; Pred. No. 2.7e-05;  
Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;  
QY 1006 CCAGATCCATGAGACCATGACCAATTCGGCGAGGATTATCACAGATTGTTTTTCGGAGG 1065  
DB 603 CCAGCTCCAGGCCACATGCAATGTCACAAGTCTGCCTTCAATGACTGTTTCAGTGGACA 662  
QY 1066 CTTGAATTACCAAGATTGACACCATTTGTGGCGACCCCTCCCTCGCCACAACCTGACAGC 1125  
DB 663 CCTCAACTTCAGATTGACACCATCTTTTCCACAGATGCTTCCACAGATGCTTCCACAA 722  
QY 1126 GGTAGTACCAGGTGGACAGCTGTGCGCAGAGCAACCTGCCGTATCGGAAACCCGCT 1185  
DB 723 AGTGCTCCCTCCCTGGTGCAGTCTTGTGTCACAGATGTCATAGATGACAGTCCCAAGCC 782  
QY 1186 GCGCATGAAGGTTGGTGCATCTGCTGCGCTATCTGCGGGTGTTCGCCCGGAT 1239  
DB 783 CTTGCTGTCAGCCTTCGCCGACATCATCCACTCACTAAAGGAGTCCAGGGCAGCT 836

Search completed: July 2, 2003, 19:28:30  
Job time : 242.694 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 13:21:06 ; Search time 1973.08 Seconds

(without alignments)

10465.482 Million cell updates/sec

Title: US-09-857-583-3

Perfect score: 1275

Sequence: 1 atttttttgcgaatgaagt.....gcgggggaaggctctataagg 1275

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	74	5.8	689	13	BJ131677
C 2	74	5.8	748	13	BJ134106
C 3	73.2	5.7	762	13	BJ128407
C 4	72.8	5.7	705	13	BJ140668
5	72.6	5.7	696	13	BJ122807
6	72.4	5.7	563	13	BJ123410

7	72.4	5.7	594	13	BJ103098
8	72.4	5.7	623	13	BJ120260
C 9	72.4	5.7	627	13	BJ155885
C 10	72.4	5.7	689	9	AU209976
C 11	72.4	5.7	704	13	BJ137106
C 12	72.4	5.7	719	9	AU213658
C 13	72.4	5.7	720	9	AU210015
C 14	72.4	5.7	721	13	BJ151779
C 15	72.4	5.7	725	13	BJ152662
C 16	72.4	5.7	727	9	AU213941
C 17	72.4	5.7	731	13	BJ149141
C 18	72.4	5.7	742	13	BJ128934
C 19	72.4	5.7	743	13	BJ128630
C 20	72.4	5.7	746	13	BJ139067
C 21	72.4	5.7	750	13	BJ148511
C 22	72.4	5.7	756	13	BJ128883
C 23	72.4	5.7	761	13	BJ129368
C 24	72.4	5.7	763	13	BJ149952
C 25	72.4	5.7	773	13	BJ153638
C 26	72	5.6	650	9	AU215555
C 27	71.4	5.6	751	13	BJ146824
C 28	71	5.6	695	13	BJ128927
C 29	70.8	5.6	550	13	BJ135898
C 30	70.8	5.6	686	13	BJ138657
C 31	70.8	5.6	720	13	BJ130441
C 32	68.8	5.4	682	13	BJ130694
C 33	68.2	5.3	625	13	BJ136773
C 34	67.6	5.3	531	9	AU222176
C 35	67.6	5.3	534	13	BJ175250
C 36	67.6	5.3	576	13	BJ141357
C 37	67.6	5.3	605	9	AU217864
C 38	67.6	5.3	607	9	AU218049
C 39	67.6	5.3	612	13	BJ138911
C 40	67.6	5.3	627	13	BJ147665
C 41	67.6	5.3	639	13	BJ134940
C 42	67.6	5.3	639	13	BJ154428
C 43	67.6	5.3	655	13	BJ144819
C 44	67.6	5.3	671	13	BJ134613
C 45	66.6	5.2	526	10	BE445712

#### ALIGNMENTS

RESULT 1  
LOCUS: BJ131677/c 689 bp mRNA linear EST 23-JAN-2002  
DEFINITION: BJ131677 unpublished oligo-capped cDNA library, C. elegans L1 stage  
Caenorhabditis elegans cDNA clone yk1057604 3', mRNA sequence.  
ACCESSION: BJ131677  
VERSION: BJ131677.1 GI:18291834  
KEYWORDS: EST.  
SOURCE: Caenorhabditis elegans.  
ORGANISM: Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoida  
; Rhabditidae; Pelodierinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 689)  
AUTHORS Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.  
and Sugano, S.  
TITLE A complementary view of the C. elegans genome  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadasu Shin-i  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
1. 689  
/organism="Caenorhabditis elegans"  
/strain="N2"  
/db\_xref="taxon:6239"





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Db      367  ATAGATGACGACCAATCTCGAATTTTAAACAACCTTCGCGCTCTTCAAATTTTGACCA 308
QY      1020 CCATGACATTCGGCGAGGATTATACAGATTGTTTTTCGAGGCTTGAATTACCAGA 1079
Db      307  CAGCAACATGACTCCATTCATTCATGATGGCTTTGGGTGGAGCTCAATATATCAGA 248
QY      1080 TTGAGCAGCATTTGTGGCGGACCTCCCTCGCCACAACCTGCAGCGGTAGCTACACAG 1139
Db      247  TCGAGCAGCAGCTGTTCACCAACANTGCCAGCTTGCAATCTGAATGCTTCATCAATATAG 188
QY      1140 TGAACAGCTGTGCCAGAGACACAACTGCCGTATC 1175
Db      187  TGAAGAATGGTGCACCAAGAAATATCTTCTTACC 152

RESULT 5
BJ122807
LOCUS      696 bp mRNA linear EST 23-JAN-2002
DEFINITION
Caenorhabditis elegans cDNA library, C. elegans L1 stage
VERSION    BJ122807
KEYWORDS   1 (bases 1 to 696)
SOURCE     Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
ORGANISM   Caenorhabditis elegans.
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE  1 (bases 1 to 696)
AUTHORS    Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE      A complementary view of the C.elegans genome
JOURNAL    Unpublished (2002)
COMMENT    Contact: Tadasu Shin-I
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.

FEATURES             source
            Location/Qualifiers
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                /organism="Caenorhabditis elegans"
                /strain="N2"
                /db_xref="taxon:6239"
                /clone="yk1292c05"
                /clone_lib="unpublished oligo-capped cDNA library, C.
                elegans L1 stage"
                /sex="hermaphrodite"
                /tissue_type="whole animal"
                /dev_stage="L1"
                /note="The AD-wrmcDNA library was generated with poly(A)+
                RNA isolated from both hermaphrodite and male N2 worms of
                all larval stages, embryos, adults and dauers and the
                subsequent generation of cDNAs by poly(A) priming. The
                cDNAs were cloned into pPC86"

BASE COUNT      225 a 131 c 144 g 196 t
ORIGIN
Query Match      5.7%; Score 72.6; DB 13; Length 696;
Best Local Similarity 57.8%; Pred. No. 1.1e-10;
Matches 129; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY      382  GTATTTCATTTGGGCGAGTGTGCTTGGGATGCATATCAACAGATGGCGTGGCTTCTCA 441
Db      469  GTATATTACTTCTGCATGTTTATTAGCACTTGCATGCGCAACAATTCGGATGGTTAACACA 528
QY      442  TGACATTTGCCACACAGACTTTCAGACCGGAACCTGCAACAACCTCGTGGGACTGGT 501
Db      529  TGAGTTCTGCGATCAACAGCAACAAGAACACACCTTTTGAATGACACTATTTCTTTGTT 588
QY      502  ATTTGGAATGGTCTGCAAGGTTTTTCCGTTGACATGTTGGAAGGACAGACAAATGCACA 561
Db      589  CTTTGGTATTTCTTACAGGATTTTCAAGAGATTTGGTGAAGGACAGCAATACACTCA 648

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QY      562  TCATTTCGGCAACCAATGTTCAAGGCGACGACCTGATATTGAC 604
Db      649  TCAGCTGCCAACAATGTAATGATCATGACGGTGATATCGAC 691

RESULT 6
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LOCUS      563 bp mRNA linear EST 23-JAN-2002
DEFINITION
Caenorhabditis elegans cDNA clone yk1299e08 5', mRNA sequence.
VERSION    BJ123410
KEYWORDS   1 (bases 1 to 563)
SOURCE     EST.
            BJT123410.1 GI:18283549
            Caenorhabditis elegans.
            Caenorhabditis elegans.
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE  1 (bases 1 to 563)
AUTHORS    Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE      A complementary view of the C.elegans genome
JOURNAL    Unpublished (2002)
COMMENT    Contact: Tadasu Shin-I
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.

FEATURES             source
            Location/Qualifiers
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                /strain="N2"
                /db_xref="taxon:6239"
                /clone="yk1299e08"
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                elegans L1 stage"
                /sex="hermaphrodite"
                /tissue_type="whole animal"
                /dev_stage="L1"
                /note="The AD-wrmcDNA library was generated with poly(A)+
                RNA isolated from both hermaphrodite and male N2 worms of
                all larval stages, embryos, adults and dauers and the
                subsequent generation of cDNAs by poly(A) priming. The
                cDNAs were cloned into pPC86"

BASE COUNT      166 a 110 c 108 g 178 t
ORIGIN
Query Match      5.7%; Score 72.4; DB 13; Length 563;
Best Local Similarity 56.2%; Pred. No. 1.1e-10;
Matches 136; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY      382  GTATTTCATTTGGGCGAGTGTGCTTGGGATGCATATCAACAGATGGCGTGGCTTCTCA 441
Db      87  GTATATTACTTCTGCATGTTTATTAGCACTTGCATGCGCAACAATTCGGATGGTTAACACA 146
QY      442  TGACATTTGCCACACAGACTTTCAGAACCGGAACCTTGGACACCTCTGTGGGACTGGT 501
Db      147  TGAGTTCTGCGCATCAACAGCGCAACAAGAACAGACCTTTGAATGATATATTTCTTTGTT 206
QY      502  ATTTGGAATGGTCTGCAAGGTTTTTCCGTCACATGTTGGAAGGACAGACACAATGCACA 561
Db      207  CTTTGGTAAATTTCTTACAGGATTTTCAAGAGATTTGGTGAAGGACAGACATAACACTCA 266
QY      562  TCATTTCGGCAACCAATGTTTCAAGGCGACGACCTTGATATTGACACACCTCCCGCCCTTACC 621
Db      267  TCAGCTTGCCACAATGTAATGATCATGACGGTGATATCGACTTGGCACCACCTTTTCGC 326
QY      622  CT 623
Db      327  AT 328

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QY 1022 ATGAACATTCGGCGAGGATTATACAGATTGGTTTTCGGAGGCTTGAATTACCAGATT 1081
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DB 330 CGCACATGACTCCATCTCCATTCATTGATGGCTTTGGGTGGACTCAATATACAGATC 271
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QY 1082 GAGCACCATTGTTGGCGACCTCCCTCGCCACACACCTGACAGCGGTAGCTTACCAGGTG 1141
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DB 270 GAGCACCATTGTTCCCAACAATGCCAGCTTGCATCTGAATGCTTGCAATGAATATGTG 211
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QY 1142 GAACAGCTGTGCCAGACACAACTGCCGTATC 1175
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DB 210 AAAGAATGGTGCAAGAGAATAATCTCCTTACC 177
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RESULT 11
BJ137106/c
LOCUS BJ137106 704 bp mRNA linear EST 23-JAN-2002
DEFINITION BJ137106 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1120e02 3', mRNA sequence.
ACCESSION BJ137106
VERSION BJ137106.1 GI:18297272
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 704)
Kohara,Y., Shin-I,T., Thlerry-Mieg,J., Thlerry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@nig.ac.jp.
Location/Qualifiers
1. 704
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1120e02"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pC86"
BASE COUNT 231 a 123 c 148 g 202 t
ORIGIN
Query Match 5.7%; Score 72.4; DB 13; Length 704;
Best Local Similarity 47.7%; Pred. No. 1.3e-10;
Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;

QY 662 CGCAAGCTCATTCAGTTCACAGACTATTTCTTGGTGCATCTGTATCTGTTCGGGTTTC 721
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DB 704 CTCGAAGATTGTACCATATCACATCTCTATTATCCCGCAATGCTTCCAAATGCTCGGTTTC 645
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DB 584 TATCAAGAAATGCATCTCTGGGACCAAGCAACAATTTGTTGGACATTTGGGCTT---GGGTA 528
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QY 842 CTGTTCACCTATTTCTTTATATGCCAGCATCCTCATCTGCTGTGGTGTGTTTTCGTTTCG 901
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Db 686 CTCAGATGTACCATATCAACATCTCTATTTCACGGCAATGCTTCCAATGCTCCGCTTC 627
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Db 626 TCATGACTGGTCACTGACGTCAATGGGTATTCAAGAGAAATCAGATGGAGTACAAGGTC 567
QY 782 TATCGCTCTCAGTATAAGAAGAGGACCAATTTGGCCTCGCCCTGCACCTGGACCTTGAAGGCC 841
Db 566 TATCAAGAAATGCATCTCTGGGAGCAAGCAACAAATTTGGACATTTGGGCTT--GGGTA 510
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AU210015 720 bp mRNA linear EST 17-JUL-2001
AU210015 unpublished oligo-capped cDNA library, stage L1
Caenorhabditis elegans cDNA clone yk751h06 3', mRNA sequence.
AU210015
EST.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
1 (bases 1 to 720)
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2001)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykoha@lab.nig.ac.jp.
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pc86"
BASE COUNT 234 a 127 c 152 g 207 t
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Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

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BJ151779 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1299e08 3', mRNA sequence.
BJ151779
EST.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
1 (bases 1 to 721)
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhini@genes.nig.ac.jp.
Location/Qualifiers
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elegans L1 stage"
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/dev_stage="L1"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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Query Match      5.7%; Score 72.4; DB 13; Length 721;
Best Local Similarity 47.7%; Pred. No. 1.3e-10;
Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
Qy 662 CGAAGCTCATTCAGTCCAGCAGTACTATTTCTGGTCACTCTATCTGTGTCGGTTC 721
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Qy 962 AAGATCGGGGACCGAGTCTGGGATGGCCATGGATTCCTGGTTGGCCAGATCCATGAGAC 1021
Db 388 AAGTATCCGCCAATTTCTCGAATTTTAACAACATTCGCCGCTCTTCAAAATTTGACCA 329
Qy 1022 ATGAACATTCGGGAGGATATACAGATGTTGTTTTCGGAGCGTTGAATACAGATT 1081
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VERSION
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KEYWORDS
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SOURCE
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  Caenorhabditis elegans.
  Rhabditidae; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
  : Rhabditidae; Peloderinae; Caenorhabditis.
  1 (bases 1 to 725)
  Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
  and Sugano, S.
  A complementary view of the C.elegans genome.
  TITLE

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JOURNAL
COMMENT
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshin@genes.nig.ac.jp.
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  /tissue_type="whole animal"
  /dev_stage="L1"
  /note="The AD-wrmcDNA library was generated with poly(A)+
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  all larval stages, embryos, adults and dauers and the
  subsequent generation of cDNAs by poly(A) priming. The
  cDNAs were cloned into pPC86"
  BASE COUNT      235 a   131 c   149 g   210 t
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Query Match      5.7%; Score 72.4; DB 13; Length 725;
Best Local Similarity 47.7%; Pred. No. 1.3e-10;
Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
Qy 562 CGAAGCTCATTCAGTCCAGCAGTACTATTTCTGGTCACTCTATCTGTGTCGGTTC 721
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Db 617 TCATGGACTGGTCAGTCAATGGGTATTTCAAGAGAGATCAATGGAGTACAAGTTC 558
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